Bos taurus Frazzle Partial human FRAZ Partial amino acid Human hsfz protein Bovine growth-indu

Amino acid sequence Mouse hafz protein Mouse ischaemic of Human ifrazzled famino acid sequence and in a series of Human ifrazzled famino acid sequence senopus growth-ind xenopus growth-ind xenopus growth-ind xenopus growth-ind wann prostate can Human prostate can Human prostate can Human frizzled-5 p prosophila melanog Human REPTR 6 prot Mouse frizzled-8 p Hydrophobic domain Mouse frizzled-7 p prosophila melanog Human frizzled-7 p prosophila melanog Human frizzled-7 p mouse frizzled-7 p mouse frizzled-4 p mouse frizzled-3 p Amino acid sequenc Human Frizzled-3 p Amino acid sequenc Mouse ifrizzled-4 p mouse frizzled-4 p

Minimum DB seq Maximum DB seq

Database

Title: Perfect score:

sednence:

OM protein

Run on:

Scoring table:

Searched:

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Breast cancer; diagnosis; prognosis; detection; screening;
antibody; oestrogen receptor; anti-oestrogen; immune response;
lymph node; metastases; tumour; BCR3; BCQ8; BCQ5; BCH1; BCN1; BCN2;
BCN5; BCO2; BCX2; BCX4; BCA2; BCX7; BCY7; BCY3; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                          AAW41253
ABB57262
AAW48695
AAW41254
AAY03229
AAW48696
AAW41251
ABP41377
AAY48252
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AAU74823
AAW31274
AAB12117
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ABB71245
AAB73308
AAB73307
AAY90903
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AAY30157.
ABB12060
AAY30156
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ABB57288
                  AAW86347
AAB48184
AAW41767
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AAW41768
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99US-0439878.
99US-04404370.
99US-0440676.
99US-0450810.
99US-0453137.
   2000WO-US06952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Breast cancer protein BCX2.
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12-NOV-1999;
12-NOV-1999;
16-NOV-1999;
16-NOV-1999;
29-NOV-1999;
02-DEC-1999;
08-MAR-2000;
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AAB00193;
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Human frizzled rel
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Human lung tumour
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1879
1 MFLSILVALCLWLHLALGVR......SPKKNIKTRSAQKRTNPKRV 346
                                                                                                         March 7, 2003, 11:19:49; Search time 38 Seconds
               5.1.3
Compugen Ltd
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                                                                                                                                                                                                                                                                                    908470 seqs, 133250620 residues
               GenCore version
Copyright (c) 1993 - 2003
                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           protein search, using sw model
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ABG61803
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WO200100828-A2
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                                                                                                  modulate breast cancer
expression profile gene
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                                                                                                                                                                                  New methods for screening drug candidates are described which comprise adding a drug candidate to a cell that expresses a protein selected from BCH1, BCA2, BCA7, BCN1, BCN3, BCA3, BCA2, BCX2, BCX2, BCX3, BCX3, BCX3, BCX3, BCX3, BCX3, BCX3, BCX3, BCX3, BCX3 and BCX3 or their fragments and determining the effect of the drug on the expression of those proteins. Antibodies to breast cancer specifically BCH1 or its fragment (BCH1p1 or BCH1p2)) are useful for inhibiting and treating breast cancer in individuals who are non-responsive to anti-oestrogen and positive for oestrogen receptor. Compositions comprising BCH1 or a nucleic acid encoding BCH1 are useful for the diagnosis and prognosis of breast cancer and for screening compositions which modulate the breast cancer phenotype. The method allows rapid and simple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human lung tumour protein related protein sequence SEQ ID NO:329
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100.0%; Score 1879; DB 21; Length 346;
Best Local Similarity 100.0%; Pred. No. 4.6e-176;
Matches 346; Conservative 0; Mismatches 0; Indels 0;
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                                                                                               Screening drug candidates for their ability to modula by contacting the drug to a cell expressing an expresand determining modulation of expression of the gene
                                                                                                                                                          Disclosure; Flg 59; 258pp; English.
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                                                                                                                                                                                                                                                                                                                                                                            detection of lymph node metastases
(EOSB-) EOS BIOTECHNOLOGY INC
                                                                      N-PSDB; AAA54127, AAA54128.
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                                                    WPI; 2000-638216/61
                                                                                                                                                                                                                                                                                                                                                                                                        346 AA;
                            Gish KC;
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cytostatic;
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                            Mack D,
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The present invention gastribes immunogenic portions of inng tumour-cassociated proteins (I) and can be used in gene therapy, antisense inhibition and in vaccines. The Nas and the lung tumour-associated proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with their inappropriate expression, especially lung cancers. For example, the NAs may be administered to.

Treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of the protein by expressing inactive proteins or to supplement the patients own production of (I). Additionally, the NAs may be used to produce the lung-tumour associated protein, according to standard recombinant DNA methodology. Conversely, antisense NA molecules may be administered to down regulate protein expression. The NA and complementary sequences may also be used as DNA probes in diagnostic and complementary sequences may also be used as antigens in the production of antibodies cancer. The (I) may be used as antigens in the production of antibodies cancer. The (I) may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of the expression and activity of the protein. Apf88083 to AAF880898 and AAF8808 represent human lung tumour protein related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes immunogenic portions of lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for preventing, diagnosing and treating lung cancer
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2000US-0533077.
2000US-0546259.
2000US-0560406.
2000US-0589184.
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17-DEC-1999;
30-DEC-1999;
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22-MAR-2000;
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05-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate timeour tissue or in prostate cancer and are derived from the tissues of various
Detecting a prostate cancer-associated transcript in a cell in a patient, useful for diagnosing prostate cancer (PC) or screening modulators of PC, by determining if prostate cancer-associated genes are expressed in a prostate issue.
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ABG61800 ABG61844 represent prostate cancer associated proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
                                                                                    SSCOCPHILPHODVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD
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                                                                                                                                                                                                                                   KKKTAGRTSRSNPPKPKGKPPAPKPASPKKNIKTRSAQKRTNPKRV 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Prostate cancer-associated protein #4.
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2000US-0733742
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2001US-281922P.
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30-APR-2001; 2001US-0847046.
04-MAY-2001; 2001US-288589P.
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N-PSDB; ABK92118.
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61 YEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWP 120
                                                                                                                                                                                                                                                     KKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLITN 240
                                                                                                                                                                                                                                                                                                                               ESCACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCKC 180
                                                                                                                                                     YEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWP 120
                                       Gaps
                                                                           1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
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Mcnabb A, Wang A, Fanger N, Switzer A, Mcneill PD, Clapper JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polynucleotide encoding a lung tumour polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein
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Length 346;
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                                       Indels
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Pred. No. 4.6e-176;
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                                         Mismatches
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100.0%;
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2000US-0677419.
2000US-0702705.
2000US-0736457.
2001US-0849626.
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2000US-0658824
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                                         Conservative
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                     Similarity
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06-OCT-2000;
30-OCT-2000;
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08-SEP-2000;
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                               The invention describes an isolated polynucleotide and polypeptide useful for stimulating and/or expanding T cells specific for a tumour protein for determining the presence of a cancer in a patient. A composition containing the presence of a cancer in a patient. A for treating a lung cancer in a patient. The polypeptide is useful for treating a lung cancer in a patient. The polypeptide is useful for removing tumour cells from a biological sample. The polynucleotide is also useful as probe or primer to detect the level of mRNA encoding a tumour protein. This is the amino acid sequence of a lung tumour associated protein, described in the method of the invention. Note: The sequence data for this patent did not form part of the polynucleoting a printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                          180
                                                                                                                                                                                                                                                                                                                                                                                          YEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWP 120
                                                                                                                                                                                                                                                                                                                                                                                                                             KKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLITN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSCQCPHILPHQDVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; phosphate homeostasis modulation; frizzled related protein-4; FRP-4; phosphate transportation; serum phosphate concentration; hypophosphataemia; phosphaturia; 1,25-dihydroxy vitamin D deficiency; osteomalacia; phosphate homeostasis related disease;
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                                                                                                                                                                                                                                                                                           1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          X-linked hypophosphataemia; rickets; oncogenic osteomalacia;
rhabdomyolysis; cardiomyopathy; tumoral calcinosis; renal failure;
bone mineralisation.
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                                                                                                                                                                                                                                 Length 346;
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100.0%; Pred. No. 4.6e-176;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human frizzled related protein 4 (FRP-4).
                                                                                                                                                                               ftp.wipo.int/pub/published_pct_sequences.
          Example 1; SEQ ID No 329; 223pp; English
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                                                                                                                                                                                                                                                      Matches 346; Conservative
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                                                                                                                                                                                                         346 AA;
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                                                                                                                                                                                                          Sequence
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The invention comprises a method for modulating phosphate homeostasis in a subject. The method involves altering the activity of the frizzled related protein-4 (FRP-4), or altering the expression of the FRP-4 gene. Phosphate plays a critical role in many cellular processes essential to normal functionality of the human body. Phosphate homeostasis is primarily regulated by the kidney, largely through variation in renal tubular re-absorption of phosphate. Alterations of the phosphate concentration often lead to serious blochemical and clinical problems. The method of the invention is useful for modulating phosphate homeostasis in a subject. The method of the invention can be used to homeostasis in a subject. The method of the invention can be used to hypophosphataemia, phosphaturia, low serum concentrations of 1.25-dihydroxy vitamin D and ostcomalacia). The method of the invention can be used to treat phosphate homeostasis-related diseases (e.g. villyed humonhamhataemia ricket concentrations of the concentration can be used to treat phosphate homeostasis-related diseases (e.g. villyed humonhamhataemia ricket concentrations of the concentration can be used to treat phosphate homeostasis-related diseases (e.g. villyed humonhamhataemia rickets concentrations of the concentration can be concentrations of the concentrations of the concentrations of the concentration can be conce
                                                                                                                                                                                                                                                                                                                                                                                                                          Modulating phosphate homeostasis in a subject, for alleviating oncogenic osteomalacia-associated symptoms, comprises altering the activity of frizzled related protein-4 (FRP4) or a gene encoding FRP-4 polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oone mineralisation). The present amino acid sequence represents the numan frizzled related protein 4 (FRP-4).
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100.0%; Pred. No. 4.6e-176;
iive 0; Mismatches 0;
                                                                                                                                                                                                                   Levine M,
                                                                                                                                                                                                                   Manavalan P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ¥.
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19-JUL-2000; 2000US-219365P,
12-JAN-2001; 2001US-261438P.
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                                                                                                                               (GENZ ) GENZYME CORP
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Matches 346; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 AA;
                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAL41901
                                                                                                                                                                                                                   Schlavi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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FRAZZLED; antiinflammatory; osteopathic; immunosuppressive; AIDS; antiarthritic; cerebroprotective; vasotropic; nephrotropic; antiHIV; cytostatic; antiarteriosclerotic; nootropic; neuroprotective; vaccine;
                                                                                                                                                                                                                           263 SSCQCPHILPHQDVLIMCYEWRSRAMLLENCLVEKWRDQLSKRSIQWEBRLQEQRRTVQD 322
                                                                                                                                                                                               241 SSCQCPHILPHQDVLIMCYEWRSRWMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New FRAZZLED polynucleotides and polypeptides useful for treating or preventing e.g. acute and chronic inflammation, autoimmune disorders, bone and cartilage diseases, cancers, or Alzheimer's disease
                                                                                                                       203 KKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLITN
  121 ESLACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCKC
                            143 ESLACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCKC
                                                                                                181 KKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLITN
                                                                                                                                                                                                                                                                                                301 KKKTAGRISRSNPPKPKGKPPAPKPASPKKNIKTRSAQKRTNPKRV 346
                                                                                                                                                                                                                                                                                                                         Claim 11; Page 11; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB48183 standard; Protein; 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUN-2000; 2000WO-US15814.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human FRAZZLED polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lark MW, James IE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-080596/09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence is the human ATG-1639 protein of the invention.

ATG-1639 is related to human secreted ligands for 7-Transmembrane receptors of the frizzled family and is homologus to Xenopus laevis Frizb protein and murine sFRP-4. ATG-1639 polypeptides and polynucleotides are useful for diagnosing susceptibility to diseases by detecting mutations in the ATG-1639 polypeptides containing the ATG-1639 mucleotide sequence, and dagnose diseases associated with ATG-1639 imbalance by determining ATG-1639 polypeptide expression levels. ATG-1639 pulpeptides can be used to screen for ATG-1639 and and and and and and and atgonists which can be used to screen for ATG-1639 and and and and and atgonists which can be used to screen for ATG-1639 activity, in addition to direct administration of antisense sequences to prevent expression, or ATG-1639 polypeptides to treat and for inducing an immune response to immunise and prevent diseases, used to affect endogenous ATG-1639 expression. ATG-1639 antibodises are used in for inducing an immune response to immunise and prevent diseases, and for isolating ATG-1639 polypeptides can be administered affinity chromatography. ATG-1639 polypeptides can be administered directly or as a vaccine to inoculate against disease. Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiovascular diseases; kidney diseases; obesity; insulin resistance; diabetes and Central Nervous System (CNS) diseases. The Affc-1639 polypeptide is also useful for mapping the gene to a chromosome, allowing gene inheritance to be studied through linkage analysis.
                                                                                                                                  Human; ArG-1639 protein; secreted ligand; 7-Transmembrane receptor;
heart disease; hypertension; cardiovascular disease; kidney disease;
obesity; insulin resistance; diabetes; Central Nervous System disorder;
therapy; sFRP-4; frizzled protein; frizb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosed, prevented or treated include: heart disease; hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid encoding ATG-1639, a human analogue of frizzled receptor ligand - useful for treatment, prevention and diagnosis of e.g. cardiovascular disease, obesity, or kidney disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 21-22; 28pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0892083.
97US-0047626.
                                                                                                                                                                                                                                                                                                                                                                                                                     97EP-0308556
                                           01-MAR-1999 (first entry)
                                                                                              Human ATG-1639 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-596873/51.
N-PSDB; AAV08951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 AA;
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                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                     27-OCT-1997;
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AAW73508;
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cancers or tumors, lymphoproliferative disorders), and and calcings and Alzheimer's disease. The polynucleotides may be used as hybridization probes for cDNA and genomic DNA, to isolate cDNA and genomic clones of other genes having high sequence similarity to the FRAZLED gene, and for chromosome identification. The polypeptides may further be used as immunospers to produce antibodies immunospersific for the FRAZLED polypeptides, as an immunological or vaccine formulation against the above cited diseases, in screening for agonists and antagonists of the adding compounds on the production of FRAZLED mRNA and protein in cells, and to identify membrane bound or soluble ligand or receptors through
The invention provides a human FRAZ2LED polypeptide. The FRAZZLED polypucled cotides and polypeptides are useful for treating chronic and acute inflammation (e.g. arthritis, osteoarthritis and other osteopenic conditions), Paget's disease, septicemia, autoimmune diseases, infection, stroke, laschemia, acute respiratory disease syndrome, renal disorders, restenosis, brain injury, AIDS (acquired immunodeficiency syndrome), metabolic and other bone diseases, cancer (e.g. bone and cartilage
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0; Gaps

Length 368; Indels 82

1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60

23 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ

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Kumar S;

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N-PSDB; AAX28656
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                                                                                                                     ESLACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCKC 180
                                                                                                                                                       KKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLITN 240
                                                                                                                                                                                                                SSCQCPHILPHQDVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD 300
                                                                                                                                                                                                                                 300
                                                           Gaps
                                                                                   1 MFLSILVALCEMEHLALGGVRGAPCEAVRIPMCRHMPWNITRMPNHEHHSTQENAILAIEQ 60
                                                                                                                                                                                       241 SSCQCPHILPHOUDVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD
                                                                           1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ
standard ligand/receptor binding techniques. The present sequence represents the human FRAZZLED polypeptide.
                                                                                                                                                                                                                                                                                                                                                                             Human frezzled-like protein; HFLP; frizzled protein family; differentiation/related disorder; agonist; antagonist; antibody; haematopolesis; wound healing; cancer; inflammatory disorder; autoimmune disease; allergic reaction.
                                                           .;
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                                          Length 346;
                                                           Indels
                                                                                                                                                                                                                                                 KKKTAGRTSRSNPPKPKGKPPAPKPASPKKNIKTRSAGKRTNPKRV 346
                                                                                                                                                                                                                                                                                                                                                            . Full length sequence of the human frezzled-like protein.
                                                 1.1e-174
                                          DB
                                         Score 1865; DE
Pred. No. 1.1e-
0; Mlsmatches
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/note= "frizzled domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note- "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "mature protein"
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                                          99.3%;
99.4%;
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                                                                                                                                                                                                                                                                                                                                              (first entry)
                                         Query Match 99.3
Best Local Similarity 99.4
Matches 344; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44..368
/note= "
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                         346 AA;
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12-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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Human: FRAZZLED protein; FRZB; chronic inflammation; acute inflammation; arthitis; osteoarthitis; septicemia; autoimmune disease; cancer; transplant rejection; graft versus host disease; infection; stroke; ischemia; acute respiratory disease syndrome; renal disorder; restenosis; brain injury; AIDS; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 YEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 SSCQCPHILPHQDVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD 300
                                                                                                                                                                           This is the amino acid sequence of the full length human frezzled-like protein (HFLP), used in the method of the invention. It is a member of the frizzled protein family. It is used in the detection and treatment of differentiation-related disorders. In conditions where HFLP is under-expressed, its agonist is involved in the treatment. Antagonist and antibodies of HFLP are used in the treatment of disorder where HFLP is over-expressed, e.g. the regulation of heematopoisis, and wound healing. HFLP products are used to develop products for treating e.g. cancers, inflammatory and autoimmune diseases, infectious diseases and allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
New isolated human frezzled-like protein - used to develop products for treating e.g. cancers, inflammatory and autoimmune diseases, infectious diseases and allergic reactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLITN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.3%; Score 1865; DB 20;
llarity 99.4%; Pred. No. 1.2e-174;
Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                         Claim 1; Fig 2A-2B; 152pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              368 AA;
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Matches 344;
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Olsen HS,
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                                                                                                                                                                                                                        Peptide
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AAY03231
              8XCCCCCCCCX8X3B15X8X8X8X8X8X8X8X8X8X8X8X833B133BX8X8X8X8X8
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                                                                                                                                                                                                                                                                                                                                                            administration of antisense sequences to prevent expression, or FRAZZLED polynucleotides to treat conditions associated with a lack of FRAZZLED protein. Gene therapy may also be used to affect endogenous FRAZZLED protein production. FRAZZLED antibodies are useful for inducing an immune response to immunise and prevent diseases, and for isolating
                                                                                                                                                                                                                                           family. The FRZB family controls signalling and developmental patterning. FRAZZLED proteins and polynucleotides are useful for diagnosing diseases related to over or underexpression of FRAZZLED protein by identifying mutations in the FRAZZLED gene, or determining FRAZZLED protein expression levels. FRAZZLED proteins can be used to screen for agonists and antagonists which bind the FRAZZLED protein by observing the binding, or stimulation or inhibition of FRAZZLED activity. These can be used in treatment to activate (agonist) or inhibit (antagonist) FRAZZLED activity, in addition to direct
                                                                                                                                                                                                                                                                                                                                                                                                                            FRAZZLED clones or purifying the protein by affinity chromatography. FRAZZLED proteins can be administered directly or as a vaccine to inoculate against diseases. Diseases diagnosed, prevented or treated include: chronic and acute inflammation, arthritis, osteoarthritis, septicemia, autoimmune diseases, transplant rejection, graft versus host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, renal disorders, restenosis, brain injury, AIDS and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 YEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESLACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCKC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLITN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSCOCPHILPHODVLIMCYEWRSRWMILENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FRAZZLED) polypeptide and polynucleotide - useful gents and for prevention and treatment of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence represents human FRAZZLED protein from the FRZB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 368;
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;; Pred. No. 2.3e-174;
1; Mismatches 2;
                                                                                                                                                                                                      Claim 11; Page 7-8; 25pp; English.
                                                              (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                as diagnostic reagents and for Alzheimer's disease and AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.1%;
99.1%;
98EP-0303163.
                        97US-0978981.
                                                                                       Lark M;
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                                                                                                              WPI; 1999-047873/05.
N-PSDB; AAV80657.
                                                                                      James I, Kumar S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 AA;
                                                                                                                                                     New FRZB -related
23-APR-1998;
                                    22-MAY-1997;
                        26-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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124 ACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCKCKKV 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated human frezzled-like protein - used to develop products for treating e.g. cancers, inflammatory and autoimmune diseases, infectious diseases and allergic reactions
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein (HFLD), used in the method of the invention. It is a member of the frizzled protein family. It is used in the detection and treatment of differentiation-related disorders. In conditions where HFLP is under-expressed, its agonist is involved in the treatment. Antagonist and antibodies of HFLP are used in the reatment of disorder where HFLP is over-expressed, e.g. the regulation of haematopoiesis, and wound healing. HFLP products are used to develop products for treating e.g. cancers, inflammatory and autoimmune diseases, infectious diseases and allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 SILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTOENAILAIEOYEE
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                                                                                                                                                                                                                                Human frezzled-like protein; HFLP; frizzled protein family; differentiation-related disorder; agonist; antagonist; antibody; demactopolesis; wound healing; cancer; inflammatory disorder; autoinmune disease; allergic reaction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is the amino acid sequence of the human frezzled-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                        Amino acid sequence of the human frezzled-like protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "frizzled domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "signal peptide"
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AAY03231 standard; Protein; 347 AA.
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97US-0055715.
                                                                                                                    (first entry)
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25..145
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                                                                                                                                                                                                                                                                                                                                                                                 Bowine; Bos taurus; frazzled protein; FR2B family; cytostatic; antiHIV; human immunodeficiency virus; nootropic; vasotropic; neuroprotective; antiInflammatory; antiarthritic; antinheumatic; immunosuppressive; cerebroprotective; antiarthritic; antisherencederic; osteopathic; ophhalmological; antipsoriatic; cartilage; bone morphogenesis; regulator; inflammation; arthritis; remematoid arthritis; osteopathic; ophthalmological; authritis; ransplant rejection; graft versus host disease; infection; tachaemia; renal disorder; restenosis; brain injury; AIDS; bone disease; osteoporosis; cancer; lymphoproliferative disorder; atherosclerosis; Alzheimer's disease; retuintis pigmentosa; macular degeneration; degenerative eye disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel Bos taurus Frazzled polypeptides and nucleotides encoding them, useful for treating inflammation, arthritis, acquired immunodeficiency syndrome (AIDS) and Alzheimer's diseases
                                             243
125 ACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCKCKKV 184
                                                                                                     244 OCPHILPHODVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEGRRTVQDKKK 303
                                                                                                                      245 QCPHILPHODVLIMCYEWRSRAMFLENCLVEKWRDQLSKRSIQWEERLQEGRRTVQDKKK 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents bovine (Bos taurus) Frazzled protein which is a member of the FRZB family. The frazzled protein can have cytostatic, antilly (human immunodeficiency virus), nootropic, vasotropic, neuroprotective, antilnflammatory, antiarthritic, antirheumatic, immunosuppressive, cerebroprotective, osteopathic, antiarteriosclerotic, ophthalmological and antipsoriatic activities, and is a regulator of cartilage and bone morphogenesis. The frazzled polynucleotide and protein are useful for treating and preventing chronic and acute inflammation, arthritis, rheumatoid arthritis, osteoarthritis, septicaemia, autoimmune diseases (e.g. inflammatory
                                                            KPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLITNSSC
                                                                                                                                                                               305 TAGRISRSNPPKPKGKTPAPKPASPKKNIKTRSAQKRTNPKRV 347
                                                                                                                                                              304 TAGRISRSNPPKPKGKPPAPKPASPKKNIKTRSAQKRINPKRV 346
                                                                                                                                                                                                                                                                                                                                                         Bos taurus Frazzled protein SEQ ID NO:2,
                                                                                                                                                                                                                                                                  AAB23911 standard; Protein; 346 AA
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bowel disease, psoriasis), transplant rejection, graft versus host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, renal disorder, restenosis, brain injury, AIDS, metabolic and other bone diseases (e.g. osteoporosis), cancer (e.g. lymphoproliferative disorders), atherosclerosis, Alzheimer's disease, retinitis pigmentosa, macular degeneration and other degenerative eye diseases. The protein pharmacokinetics in man and thus enhance compound and formulation and and in screening assays. The polynucleotide is useful for recombinant production of the frazzled protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 SSCQCPHILPHQDVLIMCYEMPSRMMLLENCLVEKWRDQLSKRSIQWEERLQEQORTAQD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ESLACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCKC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arthritis; osteoarthritis; septicemia; autoimmune disease; cancer; transplant rejection; graft versus host disease; infection; stroke; ischbemia; acute respiratory disease syndrome; renal disorder; restenosis; brain injury; AIDS; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 KKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLITN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 SSCOCPHILPHODVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD
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                                                                                                                                                                                                                                                                                                                                                                                           Length 346;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 KKRTAGRTSRSNAPKPKGKPPAPKPASPKKNIKARSAPKSTNPKQ 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 KKKTAGRISRSNPPKPKGKPPAPKPASPKKNIKTRSAQKRTNPKR 345
                                                                                                                                                                                                                                                                                                                                                                                        Ouery Match 96.2%; Score 1807; DB 21;
Best Local Similarity 95.9%; Pred. No. 5.5e-169;
Matches 331; Conservative 5; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "encoded by GAN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAWB6347 standard; Protein; 372 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Partial human FRAZZLED protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0978981.
97US-0047408.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98EP-0303163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
Misc-difference 19
                                                                                                                                                                                                                                                                                                                                   346 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP887406-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW86347;
                                                                                                                                                                                                                                                                                                                                         Sequence
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Fri Mar

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FRAZZLED; antiinflammatory; osteopathic; immunosuppressive; AIDS; antiarthritic; cerebroprotective; vasotropic; nephrotropic; antiHIV; cytostatic; antiarteriosclerotic; nootropic; neuroprotective; vaccine;
                                        Partial amino acid sequence of human FRAZZLED polypeptide.
                                                                                                                                                                                                 /label- unknown
/note= "encoded by GAN"
                                                                                                                                                                    Key Location/Qualifiers
Misc-difference 19
                                                                                                                                                                                                                                                                                                                                                           SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                    08-JUN-2000; 2000WO-US15814.
                                                                                                                                                                                                                                                                                                                                99US-0327869.
              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Lark MW, James IE,
                                                                                                                gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-080596/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     372 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AACB4496
                                                                                                                                                                                                                                          WO200075280-A2
              02-APR-2001
                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                               08-JUN-1999;
                                                                                                                                                                                                                                                                        14-DEC-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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;
                                                                                                                                                                                                                                                                                                                                              Or FRAZZLED
                                                                                                                                                                                            The present sequence represents partial human FRAZZLED protein from the FRZB family controls signalling and developmental patterning. FRAZZLED proteins and polymucleotides are useful for diagnosing diseases related to over or underexpression of FRAZZLED protein by identifying mutations in the FRAZZLED gene, or determining protein by identifying mutations in the FRAZZLED gene, or determining screen for agonists and antagonists which bind the FRAZZLED protein by observing the binding, or stimulation or inhibition of FRAZZLED activity. These can be used in treatment to activate (agonist) or inhibit (antagonist) protein addition to direct administration of antisense sequences to prevent expression, or FRAZZLE
                                                                                                                                                                                                                                                                                                                                                        polynucleotides to treat conditions associated with a lack of FRAZZLED protein. Gene therapy may also be used to affect endogenous FRAZZLED protein production. FRAZZLED attibodies are useful for inducing an immune response to immunise and prevent diseases, and for isolating
                                                                                                                                                                                                                                                                                                                                                                                                              FRAZZLED clones or purifying the protein by affinity chromatography. FRAZZLED proteins can be administered directly or as a vaccine to inoculate against diseases. Diseases diagnosed, prevented or treated include: chronic and acute inflammation, arthritis, osteoarthritis, septicemia, autokumune diseases, iransplant rejection, graft versus host disease, infection, stroke, ischaemia, acute respiratory disease syndrome, renal disorders, restenosis, brain injury, AIDS and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLIT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 CKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLIT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 NSSCQCPHILPHQDVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEGRRTVQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 NSSCOCPHILPHODYLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQ 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide and polynucleotide - useful
for prevention and treatment of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WFLSILVALCLWLHLALGVRGAP-CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DKKKTAGRISRSNPPKPKGKPPAPKPASPKKNIKTR---SAQKRINPKRV 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.9%; Score 1765; DB 20; 94.6%; Pred. No. 8.1e-165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 8.1e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB48184 standard; Protein; 372 AA
                                                                                                                                                                      Example 1; Page 11; 25pp; English.
             (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                               (FRAZZLED)
                                                                                                                                          Alzheimer's disease and AIDS
                                         Lark M;
                                                                                                                              diagnostic reagents and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 93.9
Best Local Similarity 94.6
Matches 331; Conservative
                                                                    WPI; 1999-047873/05
                                         Kumar S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                372 AA;
                                                                                                             New FRZB -related
                                                                                N-PSDB; AAV80658
                                         James I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB48184
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Kumar S;

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The invention provides a human FRAZZLED polypeptide. The FRAZZLED polynucleotides and polypeptides are useful for treating chronic and acute inflammantion (e.g. arthritis, osteoarthritis and other osteopenic conditions), Paget's disease, septicemia, autoimmune diseases, infection, stroke, ischemia, acute respiratory disease syndrome, renal disorders, crestenosis, brain injury, AIDS (acquired immunodeficiency syndrome), metabolic and other bone diseases, cancer (e.g. bone and cartilage cancers or tumors, lymphoproliferative disorders), atherosolerosis, and Alzheimer's disease. The polynucleotides may be used as hybridization of the genes having high sequence similarity to the FRAZZLED gene, and for chromosome identification. The polypeptides may further be used as immunogens to produce antibodies immunospecific for the FRAZZLED polypeptides, as an immunological or vaccine formulation against the above cited diseases, in screening for agonists and antagonists of the FRAZZLED polypeptides, to configure assays for detecting the effect of adding compounds on the production of FRAZZLED mRNA and protein in cells, and to identify membrane bound or soluble ligand or receptors through crepresents the partial FRAZZLED polypeptide sequence.
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New FRAZZLED polynucleotides and polypeptides useful for treating or preventing e.g. acute and chronic inflammation, autoimmune disorders, bone and cartilage diseases, cancers, or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MFLSILVALCLWLHLALGVRGAP-CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 MFLSILVALCLWLSPGAGRVAAPLTRSVRIPMCRHMPWNITRMPNHLHHSTQENAILAIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1765; DB 22; Length 372;
Pred. No. 8.1e-165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                       Disclosure; Page 14; 37pp; English.
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94.6%;
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35..147
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73..94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-251288/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAV18253
                                                                                                                                                                                                                                                                                                                                                                          Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9816641-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-MAR-1997;
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                                                                                                                                                                                                                                04-SEP-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В,
                                                                                                                                                                                                             AAW48694;
                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                             Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
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         123
                                              179
                                                                                                                                                                        RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents the human hsfz protein. This protein is found to increase the proliferation of neuronal cells. Such proteins can be used as nerve cell growth factors and for the detection and/or inhibition of differentiation factors, specifically those corresponding to the Drosophila melanogaster wingless or mouse int-1 type.
                  202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 CKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLIT 262
                                                                                     PESLACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCK 179
                                     180 CKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLIT 239
                                                                          240 NSSCQCPHILPHQDVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ELVDVNCSAVLRFFFCAMYAPICTLFFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPES 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding protein that increases neuronal cell proliferation - useful as nerve growth factor and for detection or inhibition of differentiation factors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSILVALCLWLHLALGVRGAPCEAVRI PMCRHMPWNITRMPNHLHHSTQENAILAIEQYE
         30;
                                                                                                                                                                                                                                                          ell growth factor; hsfz protein; neuronal cell; differentiation factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 325;
                                                                                                               DKKKTAGRISRSNPPKPKGKPPAPKPASPKKNIKIR---SAQKRINPKRV 346
                                                                                                                          323 DKKKTAGRTSRSNPPKPKGKTPAPKPASPKKNIKTRGRPTRPKRTNPKRV 372
                                                                                                                                                                                                                                                                                                                                                                                                      Risan W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Mayr T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.2%; Score 831; DB 19; 50.8%; Pred, No. 4.3e-73; 1ve 52; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                   (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                  Deutsch U, Drexler JCA, Lottspeich F,
                                                                                                                                                                               AAW41767 standard; Protein; 325 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 17; 27pp; German.
                                                                                                                                                                                                                                                                                                                                              97DE-1002835.
                                                                                                                                                                                                                                                                                                                                                                96DE-1027631
                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-088096/09.
                                                                                                                                                                                                                                        Human hsfz protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325 AA;
                                                                                                                                                                                                                                                            cell
                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAV13101
                                                                                                                                                                                                                                                          Human; nerve ce
proliferation;
                                                                                                                                                                                                                                                                                                         DE19702835-A1
                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                              27-JAN-1997;
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                                                                                                                                                                                                                      28-SEP-1998
                                                                                                                                                                                                                                                                                                                            22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                Rohrer H;
                                                                                                                                                                                                  AAW41767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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120
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                                                                                                                                                              RESULT 14
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237
                                                                                                                                         LACDELPVYDRGVCISPEAIVT----DLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bone; nerve; muscle; tumour; Wnt-expressing tumour; myodegeneration; subglottic stenosis; chondromalacia patellae; osteoarthritis; joint surface lesion; neurodegeneration; Alzheimer's disease; osteodegeneration; angiogenesis; wound healing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid encoding human, bovine and Xenopus Frzb protein and related proteins, antibodies, peptide(s), vectors and transformed cells, used to induce growth of cartilage, bone, nerve and muscle, also for inhibiting Wat-expressing tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This represents a bovine growth-inducing protein Frzb. Bovine, hume and Xenopus Frzb genes which are shown in AAV18253 to AAV18255 are
                               238 ITNSSCQCPHILPHQDVLIMCY--EWRSRMMLLENCLYEKWRDQLSKRSIQWEERLQEGR
                                                                                                             KCKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSS-SPIPRTQVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frzb; growth-inducing protein; bovine; human; Xenopus; cartilage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide cleavage site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "putative transmembrane region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
7..27
/note= "putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovine growth-inducing protein Frzb sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "N-terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "putative signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33..325
/note= "mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŝ
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                                                                                                                                                                                                                                                                                                                                    296 RTVQDKKKTAGRTSR----SNP 313
                                                                                                                                                                                                                                                                                                                                                                                     298 LSKSDSSNSDSTQSQKSGRNSNP 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW48694 standard; Protein; 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97WO-US18362.
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human and Xenopus Frzib protein sequences are shown in AAM48694 to
AAM48696. A recombinant construct containing a Frzb encoding nucleic acid
linked to a heterologous promoter in an expression vector can be used to
produce recombinant Frzb proteins. The Frzb proteins may be formulated
with fibrin glue, freeze-dried cartilage grafts or collagen (optionally
also cartilage progenitor cells, chondroblasts or chondrocytes). They
are coated on to, or mixed with, a (non-) resorbable matrix, or mixed with
a blodegradable polymer. They modulate activity of the growth factors
when it 0 8. The Frzb proteins induce skeletal morphogenesis, embryonic
pattern formation and tissue specificity and are used to induce growth
of cartilage, bone, nerve and muscle, particularly in cases of
subgloutic stemosis, chondromalacia patellae, osteoarthritis, joint
surface lesions, neurodegeneration. They also modulate Wnt-mediated
signalling in cells, and are used to inhibit growth of Wnt-expressing
tumours (particularly mammary or intestinal). The Frzb genes may also be
used to identify specific modulators or as a growth factor for cells of
the chondrocyte lineage in vitro, to stimulate wound healing, to promote
angiogenesis, to prevent transplant rejection and as adjunct to
chemotherapy or immunotherapy. Fragments of frzb proteins are used for
chemotherapy or immunotherapy. Fragments of Frzb proteins are used for
chemotherapy or immunotherapy. Fragments of Frzb proteins are used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
the frizzled gene in Drosophila. The corresponding bovine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPES 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 LACDELPVYDRGVCISPEAIVT----DLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSS-SPIPRTQVPL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 ITNSSCOCPHILPHODVLIMCY - - EWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEQR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 32; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 LLALAAALCL-LRVP-GARAAACEPVRIPICKSLDWNMTKMPNHLHHSTQANAILAIEQFE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 44.2%; Score 831; DB 19; 9
Best Local Similarity 51.4%; Pred. No. 4.3e-73;
Matches 166; Conservative 48; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296 RTVQD-----KKKTAGRTSRS 311
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Search completed: March 7, 2003, 11:23:56 Job time : 40 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

March 7, 2003, 11:23:19 ; Search time 15 Seconds
(without alignments)
678.689 Million cell updates/sec

US-09-909-775-2 1879 1 MFLSILVALCLWLHLALGVR......SPKKNIKTRSAQKRTNPKRV 346 Title: Perfect score: Sequence:

Scoring table:

262574 seqs, 29422922 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

262574

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: /cgn2_6/ptcdata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		!	Appli	Appli	Appli	Appli	Appl	Appl	Appli	Appl		Appli	Appli	Appli	Appli	Appli	Appli	Appl	Appli	Appli	Appl	Appli	Appli	Appli	Appli	Appli	Appl	Appl	Appli
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		Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMAKIES		1	78-474-7	78-474-9	78-474-3	0S-08-937-067-9	US-08-937-067-14	37-067-13	37-067-8	US-08-937-067-10	08-937-067-11	93-654B-6	93-654B-2	US-08-893-654B-4	JS-08-937-067-7	US-08-987-289-2	37-067-2	US-08-937-067-12	JS-08-937-067-6	US-08-937-067-4	US-09-233-989-10	US-08-720-484A-4	08-953-823A-4	98-239-4	US-08-720-484A-2	US-08-953-823A-2	-293-505-16	S	398-239-2
SOMM		QI .	US-08-878	US-08-878-474	US-08-878-474	.6-80-SD	.6-80-SD	US-08-937-	US-08-937-	ns-08-9	US-08-9	US-08-893-	US-08-893-	ns-08-8	08-80-SD	0S-08-9	US-08-9	08-80	0S-08-9	0S-08-9	ns-09-5	US-08-7	0S-08-6	US-09-398-2	US-08-7	0S-08-9	0S-09-5	-60	ns-00-3
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æ	Query	Match	44.2	44.1	43.4	18.0	16.2	15.9	15.6	14.0	13.6	13.2	12.4	12.2	12.1		11.6	11.5	11.0	10.6	о. О.	5.9	5.9	5.9	5.7	5.7	5.7	5.7	5.7
		Score	830	828	816	338.5	305	298.5	293	263.5	255	248	232.5	228.5	228	220	218	215.5	207	199.5	149.5	110	110	110	107	107	107	107	107
	Result	. S	1	2	3	4	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27

NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.002US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415,248-5500
TELEPA: 415,7248-5500
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:

LENGTH: 323 amino acids TYPE: amino acid TOPOLOGY: linear

TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: peptide

US-08-878-474-7 Query Match 6

Gaps

34;

44.2%; Score 830; DB 4; Length 323; 50.8%; Pred. No. 2.1e-74; Live 50; Mismatches 77; Indels

Best Local Similarity 50.8 Matches 166; Conservative

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Sequence 15, Appl Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 22, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 22, Appli	1 Inducing
US-09-293-505-15 US-08-482-677-8 US-09-136-981-2 US-08-136-981-2 US-08-136-981-2 US-08-136-981-2 US-08-136-991-2 US-08-165-259-23 US-08-665-259-23 US-08-665-259-23 US-08-1650-599A-2 US-08-152-019A-40 US-08-152-019A-26 US-08-152-019A-1	ALIGNMENTS S/08878474. s, Edward M. r, Tewis ndoderm, Cardiac and Neural actors 10 r, Parsons, Siebert & Hsue adero Center, Suite 1100 disk matible C-DoS/Ms-DoS Release #1.0, Version #1.25 RA 1997 105/08/878,474 110N:
5.7.7 5.	ឆ្ ចំពុះគ្នាស្រីស្នេស និងប្តីក្រុស និសីស
228 232 232 232 232 233 234 244 254 264 264 264 264 264 264 264 26	Sequence 7, Application U. Sequence 7, Application U. Patent No. 613322 GENERAL INFORMATION: APPLICANT: Be Wemeeste TITLE OF INVENTION: E TOWNIES: California COUNTRY: U.S.A. ZIP: 94111.4106 COMPUTER READABLE FORM MEDIUM TYPE: CIPOPY COMPUTER: IBM PC COI OPERATION SYSTEM: P SOFTWARE: PATENTIN CURRENT APPLICATION DATA APPLICATION NUMBER: FILING DATE: 18-JUN CLASSIFICATION NUMBER: FILING DATE: 20-JUN ATPORMANTING SYSTEM: P FILING DATE: 13-50.50N NAME: 51-60-17. 3

us-09-909-775-2.rai

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134 LACEELPVYDRGVCISPEAIVTADGADFPMDSS------NGNCRGASSERC 178
                                                                                                                                                                                                                                            238 ITNSSCOCPHILPHODYLIMCY - - EWRSRMMLLENCLVEKWRDOLSKRSIQWEERLOEGR 295
    16 LLALAALCL-LRVP-GARAAACEPVRIPLCKSLPWNMTKMPNHLHHSTQANAILAIEQFE 73
                                                                                                                                                                                                                        KCKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSS·SPIPRTQVPL
                                                                                                                                  LACDELPYYDRGVCISPEAIVT----DLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: De Robertis, Edward M.
APPLICANT: BOWMERSTER, Tewis
TITLE OF INVENTION: Endoderm, Cardiac and Neural Inducing
TITLE OF INVENTION: Factors
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE DALEATIN RELEASE #1.0, Version #1.25 CURRENT APPLICATION DATA:
FILING DATE: 18-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION 1966
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Majestic, Parsons, Slebert & Hsue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: Four Embarcadero Center, Suite 1100 CITY: San Francisco STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Siebert, J. Suzanne
REGISTRATION NUMBER: 28,758
REFERENCE/DOCKET NUMBER: 3100.002US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/348-5500
TELEFAX: 415/362-5418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MBDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                              296 RTVQDKKKTAGRTSR----SNP 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08878474 Patent No. 6133232
                                                                                                                                                                                                                                                                                                                                                                                                                                       298 LSKSDSSNSDSTQSQKSGRNSNP 320
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SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 161; Conservative
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Best Local Similarity
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US-08-878-474-3
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                                        238 ITNSSCQCPHILPHQDVLIMCY--EWRSRNMALLENCLVEKWRDQLSKRSIQWEERLQ--- 292
                                                                                                                                123 LACDELPVYDRGVCISPEAIVT----DLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRC 178
                                                                                                                                                                                                                                                                                                                                 238 YTTSGCLCPPLTVNEEYVIMGYEDEERSRLLLVEGSIAEKWKDRLGKKVKRWDMKLRHLG 297
                                                                                                                                                                                                                   179 KCKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSS-SPIPRTQVPL 237
16 LLVLAALCL-LQVP-GAQAAACEPVRIPLCKSLPWNMTKMPNHLHHSTQANAILAMEQFE 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: De Robertis, Edward M.
APPLICANT: Bouwmeester, Tewis
ATILE OF INVENTION: Endoderm, Cardiac and Neural Inducing
TITLE OF INVENTION: Factors
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 44.1%; Score 828; DB 4; Length 325; Best Local Similarity 50.8%; Pred. No. 3.3e-74; Matches 164; Conservative 51; Mismatches 78; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.

ZIP: 94111-4106
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Majestic, Parsons, Slebert & Hsue
STREET: Four Embarcadero Center, Suite 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Slebert, J. Suzanne
RECISTRATION NUMBER: 28,758
REFERNCE/DOCKET NUMBER: 3100.002US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/248-5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 60/020,150 FILING DATE: 20-JUN-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            293 ----EQRRTVQDKKKTAGRTSRSNPPK 315
                                                                                                                                                                                                                                                                                                                                                                                                                       298 LGKTDASDSTQNQK--SGRNSNPRPAR 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/878,474 FILING DATE: 18-JUN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08878474 Patent No. 6133232 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415/362-5418
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 325 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-JUN-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-08-878-474-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestlo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
STATE: California
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PEPTIDES ENCODED THEREBY AND
                                                                                                                      SCDRLPVLGR-----DAEVLCMDYNRSEATTAPPRPFPARPTLPGPPGAPASGGECPAG 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SILVALCLWLHLALGVRGA ---- PCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.2%; Score 305; DB 4; Length 685; 39.5%; Pred. No. 7.9e-22;
                                                                                            ACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPL----
                                                                                                                                                                                                                                                                                              Sequence 14, Application US/08937067
; Patent No. 6433155
; GENERAL INFORMATION:
   APPLICANT: Unansky, Samuil
; APPLICANT: Melkonyan, Hovsep
   TITLE OF INVENTION: A FAMILY OF GENES ENCODING
   TITLE OF INVENTION: METHODS OF USE THEREOF
; UNMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
FILING DATE:
                                                                                                                                                                      174 SPDRCKCKK-VKPTLATYLSKNYSYVIHAKIKAVQRSGC 211
                                                                                                                                                                                               186 GPFVCKCREPFVPIL-----KESHPLYNKVRTGQVPNC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119 WPESLACDELPVYDRGVCISPEAIVTD 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: MORRISON & FOERSTER
: 755 Page Mill Road
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: LeEnhardt, Susan K.
RESISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 2364
TELECOMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 685 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sin
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Best Local Similarity
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CITY: Pa
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                     64
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Patent No. 6433155
GENERAL INFORMATIOS
GENERAL INFORMATION:
APPLICANT: Unansky, Samuil
APPLICANT: Welkonyan, Hovsep
TITLE OF INVENTION: A FAMILY
TITLE OF INVENTION: APPLOSS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                 KIKAVQRSGCNEVTTVVDVKEIFKSS-SPIPRIQVPLITNSSCQCPHILPHQDVLIMCYE 260
                                                                                                                                                                                                           202 KVKEV-KVKCHDATALVEVKEILKSSLVNIPKDTVTLYTNSGCLCPQLVANEEYIIMGYE 260
                                                                                                                                                                                                                                                             261 --WRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQDKKKTAGRTSRSNPPKPKG 318
                                                                                                                                                                                                                                                                                                      -----PRKSK 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 IVTDLPEDVKWIDITPDMMVQERPLDVBCKRLSPDRCKCKKVKPTLATYLSKNYSYVIHA
ASCEPVRIPMCKSMPWNMTKMPNHLHHSTQANAILAIEQFEGLLTTECSQDLLFFLCAMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 585;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
ADDITORION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 18.0%; Score 338.5; DB 4; Best Local Similarity 33.3%; Pred. No. 3e-25; Matches 73; Conservative 37; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 494-0792
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/937,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: MORRISON & FOERSTER 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                        319 KPPAPKPASPKKNIKTRSAQ 338
                                                                                                                                                                                                                                                                                                                                                                DPVAP---IPNKNSNSRQAR 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-937-067-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 755 Page
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94304-1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-937-067-9
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Sequence 10, Application US/08937067

Patent No. 6433155
GENERAL INFORMATION:
APPLICANT: Unansky, Samuil
APPLICANT: Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APPLICANTS.TS-FEATURES PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84 ICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESLACDELPVYD-RGVCISPE-- 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEELVDVNCSAVLRFFFCAMYAP 83"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 41.7%; Pred. No. 9.4e-21;
Matches 55; Conservative 22; Mismatches 45
                                                                                                                                            APPLICATION NUMBER: US/08/937,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/937,067
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                        Floppy disk
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TITLE OF INVENTION: APOI
TITLE OF INVENTION: METH
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: 11near; MOLECULE TYPE: peptide US-08-937-067-8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 536
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-937-067-10
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           Sequence 13, Application US/08937067

Patent No. 6433155

GENERAL INFORMATION:
APPLICANT: Umansky, Samuil
APPLICANT: Umansky, Samuil
APPLICANT: Welkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES: PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
CORRESSONDENCE ADDRESS:
ADDRESSEE: MORISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 8, Application US/08937067
Patent No. 6433155
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Unansky, Samuil
APPLICANT: Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 19
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nes 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Lebnhardt. Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEPAX: (650) 849-0792
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 15.9%; Score 298.5;
Best Local Similarity 46.1%; Pred. No. 2.7e
Matches 53; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALLILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i: 572 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
US-08-937-067-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-937-067-8
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Matches
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45; Indels 10; Length 565;

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60 OYEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSW 119 : |: || || :: | : || || :: : : |
                                                                                                                                                                                                              120 PESLACDELPVYD--RGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDR 177
                                                                                                                                                                                                                                                                                                                140 PDTENCSKFPPQNDHNHMCMEGPG-----DEEVPLPHKTPIQPGEE------CHSVGSNS 188
                                                                                                                                                                                                                                                                                                                                                                                                189 DQYIWVKRSLNCVLKCGYDAGLYSRSAKEFTDIWMAVWASLC-FISTTFTVLTFLIDSSR 247
                                                                                                                                    21 LGLLLQFLLLRPTLGFGDEEERRCDPIRIAMCQNLGYNVTKMPNLVGHELQTDAELQLT 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LSILVALCLWLHLALGV---RGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GAPCEAVRIP----MCRHMPWNITRMPNHLHHSTQEN 53
                                                                                                                                                                                                                                                                                                                                                         178 CKCKKVKPTLATYLSKNYSYVIHAKI------KAVQRSGCNEVTTVVDVKEIFKSSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: RACIE, LISA, ET ALIA
TITLE OF INVENTION: FRAZZIEG NUCLEOTIDE SEQUENCES,
TITLE OF INVENTION: EXPRESSION PRODUCTS, COMPOSITIONS AND USES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                            26;
                     Length 537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 295;
                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02140-2387

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,654B
                   ; Score 255; DB 4; L; Pred. No. 5.2e-17; 49; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 248; DB 4; ; Pred. No. 1.1e-16; 48; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: GENETICS INSTITUTE,
87 CAMBRIDGEPARK DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/08893654B Patent No. 6165748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MEINERT, M.C.
REGISTRATION NUMBER: 31,544
REFERENCE/POCKET NUMBER: GI 5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,498.8574
TELEFAX: 617,876.5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.2%;
25.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      295 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 ILVALCLWLHLALGVR----
                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          230 IPRTQVPLITNSSC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248 FSYPERPIIFLSMC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                         Best Local Similarity
Matches 69; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-893-654B-6
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Best Local Sim
Matches 80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                       Query Match
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APPLICANT: Unmarsky, Samuli
APPLICANT: Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: A POPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 DVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESLAC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 NLDCSRDFRPFLCALYAPIC-MEYGRVTL-PCRRLCQRAYSECSKLMEMFGVPWPEDMEC 127
                                                                                                                                                                                                                                                                                                                                                                                                   10 LWLLTVFLGQIGGHSLFSCEPITLRNCQDLPYNTTFMPNLLNHYDQQIAALAMEPFHPMV 69
                                                                                                                                                                                                                                                                                                                                                                           11 LW-LHLALGVRGA----PCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEELV 65
                                                                                                                                                                                                                                                                                        14.0%; Score 263.5; DB 4; Length 666; 36.3%; Pred. No. 1e-17; Live 30; Mismatches 52; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126 DELP----VYDRGVCI-----SPEAIVTD----LPEDVKWIDITPDM 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 SRFPDCDEPYPRLVDLNLVGDPTEGAPVAVQRDYGFWCPRELK---IDPDL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 536
ATTORNEY/ACENT INFORMATION:
NAME: Lebnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFRENCE/POCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650),813-5600
               REFERENCE/DOCKET NUMBER: 23647-20018.00 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08937067
Patent No. 6433155
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3: MORRISON & FOERSTER
755 Page Mill Road
REGISTRATION NUMBER: 33,943
                                                      TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 494-0792
INFORMATION FOR SEQ ID NO:
                                                                                                                                             666 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               537 amino acids
                                                                                                                                                                                                                                                                                                            Best Local Similarity 36.38 Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: A FA-
TITLE OF INVENTION: APOP
TITLE OF INVENTION: METH
UNDER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                        single
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                                                                                                                                                                                                                             peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: /32
                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                STRANDEDNESS:
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                                                                                                                                                                                                                         MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-937-067-11
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                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                            Query Match
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FCDNNFA----VKVKLAKKKTTSGLHEYETEGPV-EFIKOGLLLPYDTRTMIEQWLLINE 229
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   --KPTLAT 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YLSKNYSYVIHAKIKAVQR---SGCNEVTTVVDVKEIFKSSSPIP---RTQVP--LITNS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 GLSTKCVPIPKEMAMCNDVGYSEMRLPNLLGHTNWAEVVPKSAEWQNLLQTGCHPYARTF 80
                                         190 YLSKNYSYVIHAKIKAVQR---SGCNEVTTVVDVKEIFKSSSPIP---RTQVP--LITNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08893654B
Patent No. 6165748
GENERAL INFORMATION:
APPLICANT: RACIE, LISA, ET ALIA
APPLICANT: RACIE, Frazzled NUCLECTIDE SEQUENCES,
TITLE OF INVENTION: EXPRESSION PRODUCTS, COMPOSITIONS AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65;
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                                                                                                                                                                                                                                                 242 SCQCPHI------LPHQDVLIMCYEWRSRMMLLENCLVEKW 276
                                                                                                                                                                                                                                                                                                          230 NCAOKLIRNRPTVYVIAGDIHHGKIKIFC-----SPCVLREW 266
   137 ISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCK-CKKV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/893,654B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.2%; Score 228.5; DB 4; 23.9%; Pred. No. 9.1e-15; tive 45; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: GENETICS INSTITUTE,
87 CAMBRIDGEPARK DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: MEINERT, M.C.
REGISTATION UNBER: 31,544
REFERENCE/DOCKET WUMBER: GI 52
TELECOMMUNICATION INFORMATION:
TELEFONE: 617,498.8574
TELEFAX: 617,876.5851
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     280 amino acids
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Matches 69; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: GENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02140-2387
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: CAMBRIDGE
STATE: MA
COUNTRY: USA
ZIP: 02140-2387
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                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-893-654B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
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                                      217 ILKHGSLPKTDVLPRLQQMLDLDATCVQNIMRGTRTGVYVICAEVQEGKVVVNNAYAWQK 276
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                                                                                                                     114 MYNHSWPESLACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRL 173
                                                                                                                                                                                                                                              SPDRCKCKKV-----KPTLATYLSKNYSYVIHAKIKAVQR--SGCNEVTTVVDVK-E 222
                                                                                                                                                                                                                                                                                                    161 TVPRASCRDCELEEGSTSKEILDTFCHNDFV----AKVRITKKNITSANLYDFDLDSKLE 216
                                                                                                                                                                                                                                                                                                                                                                      IFKSSS-----PIPRTQVPLITNSSCQ------CPHILPHQDVLIMCYEWRS 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77 FCANYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESLACDELPVYDRGVC 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 GLSTKCVPIPKEMAMCNDVGYSEMRLPNLLGHTNMAEVVPKSAEWONLLOTGCHPYARTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: RACIE, LISA, ET ALIA
TITLE OF INVENTION: Frazzled NUCLEOTIDE SEQUENCES,
TITLE OF INVENTION: EXPRESSION PRODUCTS, COMPOSITIONS AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73;
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SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRNT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,6548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
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24.0%; Pred. No. 3.7e-15;
Live 44; Mismatches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: GENETICS INSTITUTE, INC
STREET: 87 CAMBRIDGEPARK DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: GI 5279
TELECOMMULICATION INFORMATION:
TELEPHONE: G17.498.8574
TELEFAX: 617.876.5851
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NAME: MEINERT, M.C.
REGISTRATION NUMBER: 31,544
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INFORMATION FOR SEQ ID NO: 2:
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ZIP: 02140-2387
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
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MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION: 435
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Best Local Si
Matches 69;
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54
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Melkonyan, Hovsep
MENTION: A FAMILY OF GENES ENCODING
VVENTION: APOPTOSIS RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
VVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLPLANLECSPNIETFLCKAFVPTC-IEQIH-VVPPCRKLCEKVYSDCKKLIDTFGIRWP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | | :| | :| | | : :| | | : :| | | : :| 3 MFTFLLT--CIFLPLLRGHSLFTCEPITVPRCMKMAYNMTFFPNLMGHYDQSIAAVEMEH 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                      APPLICANT: HU, ERDING
APPLICANT: HU, ERDING
APPLICANT: ZHU, YUAN
TITLE OF INVENTION: A Human 7-TM Receptor Similar
TITLE OF INVENTION: to Murine Frizzled-6 gene
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 11.7%; Score 220; DB 2; Best Local Similarity 31.9%; Pred. No. 2.3e-13; Matches 44; Conservative 27; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/987,289
FILING DATE: 09-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GH-70060
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Patent No. 6433155
GENERAL INFORMATION:
APPLICANT: Umansky, Samuil
APPLICANT: Melkonyan, Hovsep
TITLE OF INVENTION: A FAMILY OF GI
TITLE OF INVENTION: METHODS OF USI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/048,725
FILING DATE: 02-JUN-1997
ATTORNEY/AGENT INFORMATION:
                        Sequence 2, Application US/08987289 Patent No. 5994098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 610-407-0700
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                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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EELECDRLOYCDETVPVT 136
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INFORMATION FOR SEQ ID NO:
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     610-407-0701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
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                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       19482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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US-08-937-067-2
  US-08-987-289-2
                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-987-289-2
                                                                                                                                                                                                                                                                                                           STATE:
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                                                                                                                                                                                                                              APPLICANT: Umansky, Samuil
APPLICANT: Welkonyan, Hoveen
TITLE OF INVENTION: A FAMILY OF GENES ENCODING
TITLE OF INVENTION: APOPTOSIS-RELATED PEPTIDES; PEPTIDES ENCODED THEREBY AND
TITLE OF INVENTION: METHODS OF USE THEREOF
CORRESPONDENCE: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 ---PEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCKCKKVKPTLATYLSKNY 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYVIHAKIKAVQRSGCNEVITVVDVKEIFKSSSPIPRTQVP----LITNSSCQCPHI-- 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFALRMKIKEVKKE--NGDKKIVPKKKPLKLGPIKKKDLKKLVLYLKNGADCPCHQLDN 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 AMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESLACDELPVYDRGVCIS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 PPQCVDIPADLRLCHNVGYKKMVLPNLLEHETMAEVKQQASSWVPLLNKNCHAGTQVFLC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 PCEAVRIP----MCRHMPWNITRMPNHLHHSTQENAILAIEQYEELVDVNCSAVLRFFFC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTPPNPTEASKPOGT - - - TVCP - - - - - PCDNELK - - - - - - - SEAIIEHLCAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 314;
                                 229 NCAOKLIRNRPTVYVIAGDIHHGKVKVNRVFHWQKKDSQL-TLATRRWR 276
242 SCQCPHILPHQDVLIMC------YEWRSRMMLLENCLVEKWR 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.1%; Score 228; DB 4; Length 31.
26.3%; Pred. No. 1.2e-14;
Live 45; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPHQDVLIMCYEWRSRMMLLENCLVEKWRDQLSK 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MDDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road
                                                                                                                                                               Sequence 7, Application US/08937067
Patent No. 6433155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
INFORMATION FOR SED ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 314 amino acids
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Best Local Similarity 26.3%
Matches 72; Conservative
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                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                   RESULT 13
US-08-937-067-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 LVALCLWLHLALG-----TRMPNHLHHS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 -CKRLSPD-----RCKCK-----KVKPTLATYLSKNYSYVIHAKIKAVQR-SGCNE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
11.6%; Score 218; DB 4; Length 295;
Best Local Similarity 26.3%; Pred. No. 1.1e-13;
Matches 62; Conservative 41; Mismatches 91; Indels 42;
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE:
ADDRESSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATORNEZ/AGENT INFORMATION:
NAME: Lebnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 23647-20018.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEPHONE: (650) 494-0792
INFORMATION FOR SEQ ID NO: 2:
SEQUERA: 295 and no acids
TYPE: amino acid
TOPOLICY: linear
MOLECULE TYPE: protein
US-08-937-067-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
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Search completed: March 7, 2003, 11:25:47 Job time : 17 secs

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5.1.3
Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2003
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OM protein – protein search, using sw model

7, 2003, 11:21:34 ; Search time 20 Seconds March Run on:

(without alignments)
1663.126 Million cell updates/sec

US-09-909-775-2 1879

1 MFLSILVALCLWLHLALGVR......SPKKNIKTRSAQKRTNPKRV 346 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 Total number of hits satisfying chosen parameters:

283224 seqs, 96134422 residues

Searched:

length: 0 length: 2000000000 sed Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_73:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

									_	_					_						_									
	Description	frizzled-related o	Wingless receptor			Frizzled-7 protein			Frizzled-1 protein	FZD10 protein - hu	wingless protein r				frizzled-6 protein	frizzled protein-2			membrane-type friz	collagen alpha 1(X	frizzled protein h	hypothetical prote	hypothetical prote		н	hypothetical prote		netrin-2 precursor		
SUMMARIES	ID	JC7735	S71786	JE0337	A45054	JE0339	JE0338	S03540	T25162	JC7086	T37325	JC7127	JC7312	T31690	JE0164	JE0174	JE0175	JE0315	JC7629	B56101	T13484	T46383	T34418	T21175	JC5539	S62935	F86384	B54665	E86143	
	DB	7	7	7	7	N	7	7	7	7	~	7	7	7	~	7	~	7	7	ď	N	~	~	N	N	~	~	7	~	
	Length DB	197	694	647	641	574	565	581	268	581	550	537	999	605	206	295	317	1113	579	1774	526	400	3488	651	793	965	492	581	1483	
œ	Ouery Match	55.0	17.0	16.0	16.0	15.9	15.6	15.4	15.1	15.0	14.8		14.0	12.1	11.7		11.0	10.9	8.6	7.9	6.4	5.7	5.7	5.7	5.6	5.5	5.2	5.1	5.1	
	Score	1033	319	300.5	300	298.5	293	289	283	282	279	265	262.5	226.5	220	218	207	204	162	149	120.5	107	107	106.5	105	103.5	98.5	96.5	96.5	
	Result No.	п	7	m	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	36	27	28	

wingless receptor precursor dfz2 - fruit fly (Drosophila melanogaster)
C:Speciae: Drosophila melanogaster
C:Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 02-Mar-2001
C:Accession: S71786; S78444
R:Bhanot, P.; Brink, M.; Harryman Samos, C.; Hsieh, J.C.; Wang, Y.; Macke, J.P.; Andr Nature: 382, 225-230, 1996
A:Title: A new member of the frizzled family from Drosophila functions as a wingless A:Reference number: S71786; MUID:96353971; PMID:8717036
A:Recession: S71786
A:Status: nucleic acid sequence not shown

nypormerical proce	protein UNC-89 - C	probable regulator	mitogen-activated	chemotaxis protein	transcription fact	protein kinase C	hypothetical prote	probable AraC-fami	cell surface recep	gamma-aminobutyric	acrogranin - guine	hypothetical prote	ProP effector homo	very-long-chain fa	B-cell receptor p
TSBIEB	T29757	A57376	T39306	S70180	138869	S45390	T29329	AB0337	A35103	JE0356	148141	T0007	AH0207	T52308	T18374
N	~	N	7	~	~	Н	~	~	~	7	۲,	ď	~	~	~
828	6642	1346	422	989	1104	1151	1201	261	699	960	591	1637	237	497	1030
2.0	5.0	4.9	4.9	4.9	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8	4.8
34	94	92.5	92	91.5	91	91	91	90.5	90.5	90.5	06	06	89.5	89.5	89.5

ALIGNMENTS

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C,Accession: JC7733

C,Accession: JC7733

R:Yam, J.W.P.: Chan, K.W.: Wong, V.K.W.: Hsiao, W.L.W.

Biochem. Biophys. Res. Commun. 286, 94-100, 2001

A;Reference number: JC7735; MUID:21378144; PMID:11485313

A;Accession: JC7735

A;Resciule type: DNA

A;Resciules: 1-197 <YAM>
                                                                                                                                                                                    A; Cross-references: GB: AF140347
C; Comment: This protein is a new family of secreted proteins involved in tumorigenes:
                                                                                                                                                                                                                                                                                                                        ó
          C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 14-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                         1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                          Length 197;
                                                                                                                                                                                                                                                                                      Score 1033; DB 2; Length 1
Pred. No. 1.8e-76;
1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                      Ouery Match 55.0%;
Best Local Similarity 94.9%;
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKVKPTLATYLSKNYSY 197
frizzled-related protein - rat
                                                                                                                                                                                                                                       A;Gene: rFrp
A;Introns: 148/3; 175/3
                                                                                                                                                                                                                     C; Genetics
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A; Reference number: A45054; MUID:93094228; PMID:1334084
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Best Local Similarity
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Matches
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C;Species: Rattus norvegicus (Norway rat)
C;Species: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 02-Mar-2001
C;Accession: A45054
R;Chan, S.D.; Karpf, D.B.; Fowlkes, M.E.; Hooks, M.; Bradley, M.S.; Vuong, V.; Bambino, J. Biol. Chem. 267, 25202-25207, 1992
A;Title: Two homologs of the Drosophila polarity gene frizzled (fz) are widely expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hun
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C; Species: Homo saplens (man)
C; Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
C; Accession: JE034, 6.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biophys. Res. Commun. 252, 117-122, 1998
A; Title: Molecular cloning, defferential expression, and chromosomal localization of B; Reference number: JE0337; MUID:99032814; PMID:9813155
A; Accession: JE0337
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C;Superfamily: fruit fly frizzled protein
                                                                                                                                                                                       A Molecule type: DNA
A; Residues: 1-416, Tr', 418-694 <BHW>
A; Cross-references: EMBL: U65589; NID: 91518050; PIDN: AAC47273.1; PID: 91518051
C; Genetics:
A; Gene: dfaz
A; Cross-references: FlyBase: FBgn0016797
C; Superfamily: fruit fly frizzled protein
C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         112 DLKFFLCSMYTPIC-LEDYHKPLPVCRSVCERARSGCAPIMQQYSFEWPERMACEHLPLH 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 GVPAIPKDPNLRCEEITIPMCRGIGXNMTSPPNEMNHETQDEAGLEVHQFWPLVEIKCSP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 VLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESLACDELPVY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18 GVRGAP-----CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEELVDVNCSA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24 CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEELVDVNCSAVLRFFFCAMYAP 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 ICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESLACDELPVYDRG-VCI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.0%; Score 300.5; DB 2;
1larity 45.2%; Pred. No. 1.7e-16;
Conservative 25; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 319; DB 2;
Pred. No. 5.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                 17.0%; Scor.
38.3%; Pred. No. ...
38.3%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 DRGVCISPEAIVTDLPEDVKWIDITPDMMVQERP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || : |:|
------DPDNLCMEQP 181
                                                                   A; Note: mRNA was also sequenced
R; Bhanot, P.; Wanng, Y.; Nathans, J.
submitted to the EMBL Data Library, July 1996
A; Reference number: S78444
                      A;Residues: 1-694 <BHA>
A;Cross-references: EMBL:U65589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Frizzled-1 protein - human
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-647 <SAG>
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nes 52; Conserv
                                                                                                                                                                      A; Accession: S78444
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: (05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
C; Date: (05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
C; Scossion: JE0338
B; Sagara, N.; Toda, G; Hiral, M.; Terada, M.; Katoh, M.
Biochem. Blophys. Res. Commun. 252, 117-122, 1998
A; Title: Molecular cloning, defferential expression, and chromosomal localization of A; Reference number: JE0338
A; Title: Molecular Cioning, MulD: 99032814; PMID: 9813155
A; Accession: JE0338
A; Status: preliminary
A; Molecule type: mRNA
A; Molecule type: MRNA
A; Residues: 1-565 < SAG>
A; Cross-references: DDBJ: AB017364; NID: 93927884; PIDN: BAA34667.1; PID: 93927885
C; Superfamily: fruit fly frizzled protein
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A;Realdudes: 1-774 <SRO.
A;Crosa-references: DDBJ.AB017365; NID:g3927886; PIDN:BAA34668.1; PID:g3927887
C;Superfamily: fruit fly frizzled protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 02-Mar-2001
C;Accession: JE0339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 ILLWILEAPLILGVRAQPAGQVSGPGQQRPPPPQPQGGGQQYNGERGISIPDHGYCQPIS 115
                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29 IPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEELVDVNCSAVLRFFFCAMYAPICTLE
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                                                                                                                                                                                                                                                                                                                                    44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 FLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESLACDELPVYDRG-VCI 137
                                                                                                                                                                                                                                                                 Length 641;
A;Status: preliminary; not compared with conceptual translation A;Molecule type: nucleic acid A;Residues: 1-641 <CHA>
A;Residues: 1-641 <CHA>
A;Experimental source: UNR 106 osteosarcoma cell line A;Note: sequence extracted from NCBI backbone (NCBIP:120154)
C;Superfamily: fruit fly frizzled protein
                                                                                                                                                                                                                                                                                                                                       Indels
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A;Tille: Molecular cloning, defferential expression, and A;Reference number: JE0337; MUID:99032814; PMID:9813155
A;Recession: JE0339
A;Status: preliminary
                                                                                                                                                                                                                                                     16.0%; Score 300; DB 2; Lv 36.5%; Pred, No. 1.9e-16;
tive 26; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                              9 LCLWL --- HLALGVRGAP-----
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Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                       Conservative
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1. 2.

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A; Experimental source: clone T2308
R;Rocheleau, C.E.; Downs, W.D.; Lin, R.; Wittmann, C.; Bei, Y.; Cha, Y.H.; Ali, M.; P Cell 90, 707-716, 1997
A;Title: Wnt signaling and an APC related gene specify endoderm in early C. elegans e A;Reference number: Z15051; MUID:97433081; PMID:9288750
A;Accession: T42210
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JG7086
FZD10 protein - human
C;Species: Homo sapiens (man)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Mar-2001
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Mar-2001
C;Accession: JG7086
B;Koike, J.; Takagi, A.; Miwa, T.; Hirai, M.; Terada, M.; Katoh, M.
Biochem. Biochem. Biophys. Res. Commun. 262, 39-43, 1999
A;Fitle: Molecular cloning of Frizzled-10, a novel member of the Frizzled gene family A;Reference number: JG7086; MUID:99382237; PMID:10448064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-568 <ROC>
A;Residues: 1-568 <ROC>
A;Cross-references: EMBL:AF013953; NID:g2463673; PIDN:AAC47750.1; PID:g2463674
                                                                                                                                                                              A Status: preliminary; translated from GB/EMBL/DDBJ
A) Molecule type: DNA
A; Residues: 1-568 GWIL>
A; Cross-references: EMBL:281128; PIDN:CAB03398.1; GSPDB:GN00019; CESP:T23D8.1
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A;Map position: 12q24.33
G;Nuperfamily: fruit fly frizzlèd protein
C;Keywords: glycoprotein; lung; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 283; DB 2;
Pred. No. 3.9e-15;
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C; Superfamily: fruit fly frizzled protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                    submitted to the EMBL Data Library, October 1996
A;Reference number: 219989
A;Accession: 725162
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Best Local Similarity
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Les 57; Conserv
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A; Residues: 1-581 <KOI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene frizzled protein precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: Drosophila melanogaster
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 02-Mar-2001
C;Accession: 803540; 815708; 815708
R;Vinson, C.R.; Conover, S.; Adler, P.N.
Nature 338, 263-264, 1989
A;Title: A Drosophila tissue polarity locus encodes a protein containing seven potential
A;Reference number: 803540; MUID:89159415; PMID:2493583
A;Accession: 803540
A;
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Genetics 12b, 401-41b, 1990
Genetics Molecular structure of frizzled, a Drosophila tissue polarity gene. A; Reference number: S15708; MuID:91060073; PMID:2174014
A; Accession: S15708
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-581 <ADL>
A; Accession: S15709
A; Accession: S15709
A; Accession: S15709
A; Accession: S15709
A; Molecule type: DNA
A; Residues: 1-405, WY, 408, WOFHTIN' <AD2>
A; Cross-references: EMBL:X54648; NID:97973; PIDN:CAA38461.1; PID:9804980
A; Cross-references: EMBL:X54648; NID:97973; PIDN:CAA38461.1; PID:9804980
A; Cross-references: EMBL:X54648; NID:97973; PIDN:CAA38461.1; PID:9804980
A; Cross-references: FlyBase:FBan0001085
F; Cross-references: FlyBase:FBan0001085
F; T-26/Domain: signal sequence **status predicted <SIG>F; 27-581/Product: gene frizzled protein **status predicted <MAT>F; 27-581/Product **status predicted <MAT>F; 27-581/Product **status predicted <MAT>F; 27-581/Product **status predi
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C;Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *text_change 02-Mar-2001
C;Accession: T25162; F42110
                                                                                                                                                                                                                                                                                                                                               84 ICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESLACDELPVYD-RGVCISPE-- 140
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                  24 CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEELVDVNCSAVLRFFFCAMYAP 83
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                 Length 565;
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15.6%; Score 293; DB 2; L 41.7%; Pred. No. 6e-16; Live 22; Mismatches 45;
                                                                                           Conservative
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                                                        Local Similarity
                 Query Match
                                                        Best Loc
Matches
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frizzled-3 (FZD3).
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C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Accession: T31690
R:Wamsley, P.; Reppler, D.
R:Reference number: 221069
A;Reference number: DNA
A;Residues: 1-605 <WAM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo saplens (man)
C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 02-Mar-2001
C;Accession: JC7312
                                                                        116 NHSWPESLACDELPVYD--RGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRL 173
                                                                                                                                                                                                                                                                                  136 GFAWPESLNCSKFPPQNDHNHMCMEGPG-----DEEVPLPHKTPIQPGEB-----CHSV 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status C.F.; Formentl, E.; Terstappen, G.C.; Caricasole, A.
Blochen Blophys. Res. Commun. 273, 27-34, 2000
A;Title: Identification, gene structure, and expression of human frizzled-
A;Reference number: JC7312
A;Accession: JC7312
A;Accession: JC7312
A;Accession: JC7312
A;Accession: Jc66 < SAL>
A;Cross-references: GB:AJ27242
A;Cross-references: GB:AJ27242
A;Cross-references: Brain
C;Comment: This protein, a seven-transmembrane receptor belonging to the foositol levels in cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 IVFSLWPLTVFMGHIGGHSLFSCEPITLRMCQDLPYNTTFMPNLLNHYDQQTAALAMEDF 65
17 VGLSLGLLLQLLLLLGPARGFGDEEERRCDPIRISMCQNLGYNVTKMPNLVGHELQTDAE 76
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                                                 56 LAIEQYEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMY
                                                                                                                                                                                                                                                   174 SPDRCKCKKVKPTLATYLSKNYSYVIHAKI ••••**KAVQRSGCNEVTTVVDVKEIFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 SLACDELP----VYDRGVCI-----SPEAIVTD----LPEDVKWIDITPDM 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
A; Gene: fad3
A; Map position: 8p21
C; Superfamily: fruit fly frizzled protein
C; Superfamily: fruit cupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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Matches 61; Conserv
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                                                                                          wingless protein receptor Cfz2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 [sequence_revision 03-Dec-1999 #text_change 02-Mar-2001
C;Accession: T37325
R;Sato, A.; Kojima, T.; Ui-Tei, K.; Miyata, Y.; Saigo, K.
Development 126, 4421-4430, 1999
A;Title: Dfrizzlad-3, a new Drosophila Wnt receptor, acting as an attenuator of Wingless A;Reference number: 221689; MUID:99429803; PMID:10498678
A;Accession: T37325
A;Status: preliminary; translated from GB/EWBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                 A; Molecule Lyper. DNA A; MOLECULE A. MOLECULE A. MOLECULE A; MOLECULE A; Residues: 1-550 <SAT>
A; Cross-references: EMBL: AB026113; NID: 95931529; PIDN: BAA84678.1; PID: 95931530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Status: preliminary
A.Molecule type: mRNA
A.Rosidues: 1-537 <KIR>
A.S.COSS-references: GB:AB032417; DDBJ:AB032417; NID:g6277265; PID:g6277266
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 ILAIEQYEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKM 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: Cf22
C; Superfamily: fruit fly frizzled protein
C; Keywords: receptor; signal transduction; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 14.8%; Score 279; DB 2; Length 550; Local Similarity 30.7%; Pred. No. 7.9e-15; los 75; Conservative 32; Mismatches 89; Indels
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Best Local Similarity 28.7%; Pred. No. 1e-13;
Matches 74; Conservative 47; Mismatches 107; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 YNHSWPESLACDELP----VYDRGVCISPEAIVTDLP-----
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C;Superfamily: fruit fly frizzled protein
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Matches
                                              RESULT 10
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Ritu, E.; Zhu, Y.; Fredrickson, T.; Barnes, M.; Kelsell, D.; Beeley, L.; Brooks, D. Biochem. Biophys. Res. Commun. 247, 287-293, 1998
A;Title: Tissue restricted expression of two human frzbs in preadipocytes and pancrea A; Reference number: JEO174; MUID:98308108; PMID:9642118
A;Roccession: JEO174
A;Rocious type: mRNA
A;Rocious type: mRNA
A;Rocious: 1-295 <HUA>
C;Genetics: A;Rap position: 4q
                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 07-May-1999
C;Accession: JE0174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50 IQENAILAIEQYEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCE 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91; Indels 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.6%; Score 21%; DB 2; Best Local Similarity 26.3%; Pred. No. 3.4e-10; Matches 62; Conservative 41; Mismatches 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: March 7, 2003, 11:25:27 Job time: 23 secs
     119 EELECDRLQYCDETVPVT 136
                                                                                                                                          frizzled protein-2 - human
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Blochem. Blophys. Res. Commun. 243, 622-627, 1998
A:Title: Molecular cloning of human frizzled-6.
A:Reference number: JE0164; MUID:98153814; PMID:9480858
A:Accession: JE0164
A:Molecule type: mRNA
A:Kesidues: 1-706 <TOK>
A:Kesidues: 1-706 <TOK>
A:Cross-references: GB:AB012911; NID:93062802; PIDN:BAA25686.1; PID:93062803
C;Comment: This protein is receptor for selected glycoproteins in development and carcing G:Genetics:
A;Cross-references: EMBL:AF016413; PIDN:AAB65257.1; GSPDB:GN00023; CESP:F27E11.3
A;Experimental source: strain Bristol N2; clone F27E11
C;Genetics:
                                                                                                                                                                                                                                                                         7 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Date: 03-Jul-1998 *sequence_revision 10-Jul-1998 *text_change 02-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                 99 SVCQRARDDCEPLMKMYNHSWPESLACDELP-----VYDRGVCISPEAIVTDLP----- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 ------EDVKWIDITPDMMVQERPLDVDCKRLSPDRCKCKKVKP--TLATYLSK- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 HHHKNQNQNQNUNNYSPDGPEVGISKIDNEVIA---GPSECQCTCNQPFQFVASEKSKV 172
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                                                                                                                                                                                                                                                                                                                                                          37; Gaps
                                                                                                                                                                                                                                                                                                                        39 ITRMPNHLHHSTQENAILAIEQYEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCK 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Map position: 8422.3-q23.1
C.Superfamily: fruit fly frizzled protein
C.Keywords: 91ycoprotein
C.Keywords: 91ycoprotein
F.1-18/Pomain: signal sequence #status predicted <SIG>
F.201-222/Domain: transmembrane #status predicted <TM1>
F.231-255/Domain: transmembrane #status predicted <TM2>
F.281-312/Domain: transmembrane #status predicted <TM3>
F.381-312/Domain: transmembrane #status predicted <TM4>
F.374-345/Domain: transmembrane #status predicted <TM4>
F.374-345/Domain: transmembrane #status predicted <TM4>
F.471-436/Domain: transmembrane #status predicted <TM6>
F.473-495/Domain: transmembrane #status predicted <TM6>
F.473-495/Domain: transmembrane #status predicted <TM6>
F.473-495/Domain: transmembrane #status predicted <TM6>
F.381-382/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                      Length 605;
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                                                                                                                                                                                          Score 220; DB 2;
Pred, No. 6,4e-10;
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31.9%; Pred. No. v...
                                                                                                                                                                                                             Ouery Match 12.1%; Score 226.5;
Best Local Similarity 29.5%; Pred. No. 1.6e
Matches 59; Conservative 27; Mismatches
                                                                            A,Gene: CESP:F27E11.3
Map position: 5
A:Introns: 28/3; 454/1; 520/1; 562/1
C;Superfamily: fruit fly frizzled protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           frizzled-6 protein precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 ----NYSYVIHAKIKAVQRS 209
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Best Local Similarity
Matches 44; Conserva
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us-09-909-775-2.rsp

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                - protein search, using sw model
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OM protein

March 7, 2003, 11:20:34 ; Search time 13 Seconds Run on:

(without alignments)
1103.908 Million cell updates/sec

US-09-909-775-2 1879

1 MFLSILVALCLWLHLALGVR.....SPKKNIKTRSAQKRTNPKRV 346 Title: . Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID		
1	831	44.2	325	7	FRZB_BOVIN	095117 bos taurus	
7	830	44.2	323	г	FRZB_MOUSE	1 mus muscu	
e	828	44.1	325	-	FRZB_HUMAN	Q92765 homo sapien	
4	338.5	٠	585	~	F2D5_HUMAN	7 homo	
S	331		577	H	FZD5_MOUSE	mus m	
9	318	•	694	Н	FRZ2_DROME	3 dro	
7	312	•	591	~	F2D9_HUMAN	-	
89	310	16.5	592	_	FZD9_MOUSE	mus n	
6	308.5		549	_	F2D7_XENLA		
10	308	16.4	694	Н	F2D8_HUMAN		
11	307.5	•	642	-	F2D1_MOUSE	mus	
12	306		567	-	F2D7_CHICK	qal	
13	306		581	-	FZD8_XENLA	xenopus	
14	305.5		592	,	F2D1_CHICK	-	
15	305	•	685		FZD8_MOUSE		
16	303		559		FZD1_XENLA	Q9i9m5 xenopus lae	
17	301.5		559	Н	FZD5_XENLA		
18	300.5		648		F2D1_HUMAN	homo sap	
19	299.5	•	574	Н	F2D7_HUMAN	homo	
20	299	15.9	583	Н	FRIZ_DROVI	drosc	
21	298.5		572	-	FZD7_MOUSE		
22	294	15.	641	-	FZD1_RAT	Q08463 rattus norv	
23	293.5	15.	. 551		F2D2_XENLA	Ogpuu6 xenopus lae	
24	293.5	15.	580	-	FZ0B_XENLA	O9w742 xenopus lae	
25	293	15.	565	, - 1	FZD2_HUMAN	Q14332 homo sapien	
56	293	15.	570	-	FZD2_MOUSE	_	
27	293	15.	570	-	FZD2_RAT		
28	292	15.	585	7	F210_CHICK	Q9pwh2 gallus gall	
53	289	15.	581	-	FR12_DROME	drosop	
30	287.5	Н	523	Н	FZD2_CHICK		
31	285.5	15.	586	_	FZ0A_XENLA	xenopus	
32	282	15.0	581	-	F210_HUMAN	homo sap	
33	271.5	14.4	523	П	FZD4_XENLA		

265 14.1 537 1 FZD4_HUMAN 262.5 14.0 666 1 FZD3_MOUSE 262.5 14.0 664 1 FZD3_KENLA 262.5 14.0 666 1 FZD3_HUMAN 260 13.8 525 1 FZD4_CHTCK 259 13.8 538 1 FZD4_CHTCK 259 13.6 537 1 FZD4_MOUSE 220 12.1 705 1 FZD4_MOUSE 220 11.7 705 1 FZD6_MOUSE 215.5 11.5 709 1 FZD6_MOUSE 215.5 11.4 1042 1 CORT_HUMAN 204 10.9 1113 1 CORT_MOUSE	1 22 B BOVI 25 B BOVI 55117; 1-0CT - 20 OUN - 20 - 1zzled - 22 25 OR F	Bos taurus (Bovine). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Bovinae; Bos. NCBI_TaxID=9913; [1] SEQUENCE FROM N.A. TISSUE-Cartilage; MEDLINE-96421609; PubMed-8824257; MEDLINE-96421609; PubMed-8824257; MEDLINE-96421609; PubMed-8824257; Primary structure and tissue distribution of FRZB, a novel protein related to Drosophila frizzled, suggest a role in skeletal "J. Biol. Chem. 271:26131-26137(1996).	ILERACTION BETWEEN THE IDLINE-97470942; PubMed IN Wang S., Julius N. Watl. Acad. Sci. U. Cor. Mall. Acad. Sci. U. S. Watl. Acad. Sci. U. SUBCELLULAR ILCATION. AS SOLUBLE WAY SUBCELLULAR ILCATION. DOMAIN: The FZ domai. SUBCELLULAR ICCATION. DOMAIN: The FZ domai. SIMILARITY: CONTAINS. SIMILARITY: CONTAINS STASS-PROT entry is the European Bioinformate by non-profit insudicines requires a lice send an email to lice send an email to lice such acad.	Interpro; IPR000024; Fz_domain. Interpro; IPR00134; Netrin_C. Pfam; PF01392; Fz; 1. SMART; SM00063; FR; 1. SMART; SM00063; FR; 1. Glycoprotein; Signal. SIGNAL 32 POTENTIAL. CHAIN 33 325 FRIZZLED-RELATED PROTEIN.
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MEDILINE-97250455; Pubmed-9096311;
Rattner A., Haish J.C., Smallwood P.M., Gilbert D.J., Copeland N.G.,
Jenkins N.A., Nathans J.;
A family of secreted proteins contains homology to the cysteine-rich
Ligand-binding domain of frizzled receptors ";
Proc. Natl. Acad. Sci. U.S.A. 94:2859-2863(1997).
                                                                                                                                                                                                                                                  ELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPES 122
                                                                                                                                                                                                                                                                                              123 LACDELPVYDRGVCISPEAIVT----DLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRC 178
                                                                                                                                                                                                                                                                                                                            -----NGNCRGASSERC 178
                                                                                                                                                                                                                                                                                                                                                                                                                       ITNSSCQCPHILPHQDVLIMCY - - EWRSRAMLLENCLVEKWRDQLSKRSIQWEERLQEQR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                    3 LSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYE 62
                                                                                                                                                                                      Leyns L., Bouwmeester T., Kim S.H., Piccolo S., De Robertis E.M.;
FFTsD-1 is a secreted antagonist of Wnt signaling expressed in the
Spenann organizer ":
                                                                                                                                                                                                                                                                                                                                                             KCKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSS-SPIPRTQVPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
FZ.
NTR.
SER-RICH.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
39E337A9C6E98BB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRZB_MOUSE STANDARD; PRT; 323 AA.
P97401; 009075; 009093;
16-0CT-2001 (Rel. 40, Crated)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Frizzled-related protein precursor (Frzb-1) (Frezzled) (Fritz)
Secreted frizzled-related sequence protein 3) (SFRP-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mayr T., Deutsch U., Kuehl M., Drexler H.C.A., Lottspeich F., Deutzmann R., Wedlich D., Risau W.; **Fritz: a secreted frizzled-related protein that inhibits Wnt
                                                                                                         Length 325;
                                                                                                         ; Score 831; DB 1; Length 32; Pred. No. 3.1e-62; 48; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                           134 LACEELPVYDRGVCISPEAIVTADGADFPMDSS----
                                                                                                       11arity 51.4%; Score 831; 11arity 51.4%; Pred. No. 3 Conservative 48; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-97236495; Pubmed-9118218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 RTVQD-----KKKTAGRTSRS 311
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                                                                           36234 MW;
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318
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Cell 88:747-756(1997).
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                                           49
299 2
325 AA;
                                                                                                                         Similarity
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Matches 166;
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CARBOHYD
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FRZB_MOUSE
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                                              Arakawa T., Hara A., Fukunishi Y., Koshino M., Itoh M., Ishili Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alizawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Raito T., Okazaki Y., Goldbori T., Bono H., Kasukawa T., Salto R., Kadota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T., Ruchi P., Lewis S., Matsuo Y., Mikaldo I., Pesole G., Ouackenbush J., Schrim I.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washlo T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bersh G., Blake J., Boffelli D., Bojunga N., Carninch P., de Bonaldo M.F., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchlonni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wishbaw-Balla M., Weitz C., Whittaker C., Wilming L., Wayshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLUIAR LOCATION: Secreted (Probable).
-!- DOMAIN: The FZ domain is involved in binding with Wnt ligands (By similarity).
-!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
-!- SIMILARITY: CONTAINS 1 NTR DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13 LACDELPVYDRGVCISPEAIVT----DLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 LUVLAALCL-LQVP-CAQAAACEPVRIPLCKSLPWNWTKMPNHLHHSTQANAILAMEQFE 73
                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection."; Nature 409:689-590(2001).
-1- FUNCTION: MAY BINYOLVED IN MORPHOGENESIS OF SKELETON. MAY ACT AS A SOLUBLE WNT-BINDING PROTEIN THAT MAY ANTAGONIZE WNT
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FRIZZLED-RELATED PROTEIN.
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                STRAIN-C57BL/6J; TISSUE-Tongue;
MEDLINE-21085660; PubMed-11217851;
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InterPro; IPR001134; Netrin_C.
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PROSITE; PS50038; FZ; 1.
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Pfam; PF01759; NTR; 1.
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165
301
49
323 AA;
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                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
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Matches 166;
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CARBOHYD
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Homo sapiens
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Q13467;
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ID FZDS_HUMAN

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TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN THE CARTILAGENOUS CORES OF THE LONG BONE DURING EMBRYONIC AND FETAL DEVELOPMENT AND IN THE APPENDICULAR SKELETON (6-13 WEEKS). AT 13 WEEKS OF GESTATION, TRANSCRIPTS WERE PRESENT IN EARLY CHONDROBLASTS OF THE TARSAL BONES OF THE FOOT, THE CARPAL BONES OF THE HANDS AND THE EPIPHYSIS OF LONG BONES. HIGHLY EXPRESSED IN PLACEMTA AND HEART, FOLLOWED BY BRAIN, SKELETAL MUSCLE, KIDNEY AND PANCREAS. WEAKLY EXPRESSED IN
              ------1GHCRGASSERC 178
                                                                                            238 ITNSSCQCPHILPHQDVLIMCY - - EWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQ - - . 292
                                                                                                          DOMAIN: The F2 domain is involved in binding with Wnt ligands (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spemann organizer.";
Cell 88:747-756(1997).
-!- FUNCTION: MAY BE INVOLVED IN MORPHOGENESIS OF SKELETON. MAY ALSO
ACT AS A SOLUBLE WNT-BINDING PROTEIN THAT MAY ANTAGONIZE WNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hoang B., Moos M. Jr., Vukicevic S., Luyten F.P.;
"Primary structure and tissue distribution of FRZB, a novel protein related to Drosophila frizzled, suggest a role in skeletal morphogenesis.";
J. Biol. Chem. 271:26131-26137(1996).
                                                     KCKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSS-SPIPRTQVPL
                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                          092765; 000181; 099686;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Frizzled-related protein precursor (Frzb-1) (Frezzled) (Fritz).
FRZB OR FRZBI OR FRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97236495; PubMed-9118218;
Leyns L., Bouwmeester T., Kim S.-H., Piccolo S., de Robertis E.
"Frzb-1 is a secreted antagonist of Wnt signaling expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mayr T., Deutsch U., Kuehl M., Drexler H.C.A., Lottspeich Deutzmann R., Wedlich D., Risau W.; **Fritz: a secreted frizzled-related protein that inhibits
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
-!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
-!- SIMILARITY: CONTAINS 1 NTR DOMAIN.
                                                                                                                                                                                                                                                   325 AA.
----EQRRTVQDKKKTAGRTSRSNPPK 315
                                                                                                                                                                 298 LGKTDASDSTQNQK--SGRNSNPRPAR 322
                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96421609; PubMed-8824257;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 KCKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSS-SPIPRTQVPL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 LEALAALCL-LRVP-GARAAACEPVRIPICKSLPWNWTKMPNHLHHSTQANAILAIEQFE 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   .) (POTENTIAL).
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non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.1%; Score 828; DB 1; Length 325
50.8%; Pred. No. 5.4e-62;
Live 51; Mismatches 78; Indels
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Frizzled 5 precursor (Frizzled-5) (Fz-5) (HFz5) (FzE5).
FZD5 OR HFZ5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .) (PV
A -> D (IN REF. 2).
K -> N (IN REF. 1).
8337C51BBA9A4B07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                    FRIZZLED-RELATED PROTEIN
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MEDLINE*96224032; PubMed=8626800;
                                                                                                                                                                         MIM; 605083; -.
InterPro; IPR000024; Fz_domain.
InterPro; IPR001134; Netrin_C.
Pfam; PF01192; Fz; 1.
Pfam; PF01759; NTR; 1.
SWART; SM00063; FRI; 1.
PROSITE; P55038; FZ; 1.
Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296 RTVQDKKKTAGRTSR----SNP 313
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150
294
318
318
63
106
85
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87
36254 MV;
                                                                                             EMBL; U24163; AAC50736.1; -. EMBL; U91903; AAB51298.1; -. EMBL; U68057; AAC51217.1; -. Genew, HGNC:3959; FRZB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 164; Conservative
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Mammalia; Eutheria;
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106
325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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33
165
301
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Science 275:1652-1654(1997).

**Control Receptor for Whit proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of wir target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway. Sp PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and interrecellular transmission of polarity.

**Control of the control of the proteins of the control of the pathway is seen to information during itssue morphogenesis and/or in differentiated this were specifically with Wnt5A to Induce the beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright, It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             catenin pathway.

SUBCELLUIAR LOCATION: Integral membrane protein.

DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of the Wnt/Dotta-catenin signaling pathway (By similarity).

DOMAIN: The fz domain is involved in binding with Wnt ligands (By
                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUPLING TO BETA-CATENIN PATHWAY.
MEDLINE-97207341; PubMed-9054360;
He X., Saint-Jeannet J.P., Wang Y., Nathans J., Dawid I., Varmus H.;
"A member of the Frizzled protein family mediating axis induction by
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                                                                                                                                                        MEDLINE=21301556; PubMed=11408929; Saitch T., Hiral M., Katch M.; Mulecular cloning and characterization of human Frizzled-5 gene of chromosome 2933.3-934 region."; Int. J. Oncol. 19:105-110(2001).
                                                                                                                                                                                                                                                                                                                TISSUE-Oesophageal carcinoma;
MEDLINE-9837433; PubMed-9707618;
Tanaka S., Akiyoshi T., Mori M., Wands J.R., Sugimachi K.;
Anovel firizzled gene identified in human esophageal carcinoma mediates AFC/beta-carcenin signals.";
Proc. Natl. Acad. Sci. U.S.A. 95:10164-10169(1998).
Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.; A large family of putative transmembrane receptors homologous product of the Drosophila tissue polarity gene frizzled."; J. Biol. Chem. 271:4468-4476(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
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PROSITE; PSS0261; G_PROTEIN_RECEP_F2_4; 1.
Multigene family; G-protein coupled receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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InterPro; IPR000539; Frizzled.
InterPro; IPR000024; Fz_domain.
InterPro; IPR000832; GPCR_secretin.
                                                                                                                                                                                                                                                                                              SEQUENCE OF 273-331 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U43318; AAC50385.1; -. EMBL; AB043702; BAB60959.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01392; Fz; 1.
Pfam; PF01534; Frizzled; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0489; FRIZZLED.
SMART; SM00063; FRI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGNC:4043; FZD5
                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 1 1 1 1
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Ishikawa T., Tamai Y., Zorn A.M., Yoshida H., Seldin M.F., Nishikawa S.-T., Taketo M.M.; "Mouse Wnt receptor gene Fzd5 is essential for yolk sac and placental anglogenesis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                            LVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                       .24 ACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPL-------DVDCKRL 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCDRLPVLGR-----DAEVLCMDYNRSEATTAPPRPFPAKPTLPGPPGAPASGGECPAG 185
                                                                                                                                                                                                                                                                                                                                                                                            ILVALCLWLHLALGVRGAP-CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEE 63
                                                                                                                                                                                                                          N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
T -> S (IN REF. 2).
DT -> BR (IN REF. 2).
A -> G (IN REF. 2).
G -> A (IN REF. 2).
R -> G (IN REF. 2).
R -> G (IN REF. 2).
R -> G (IN REF. 2).
W. CF6GCSBA746E7971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                         25;
                                                                                                                                                                                                                                                                                                                                  Length 585;
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                   4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
        FRIZZLED 5.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                 6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                       2 (POTENTIAL)
EXTRACELLULAR (POTENTIAL)
                                                                             3 (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
                                                                                                                         5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                        7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                          LYS-THR-X-X-X-TRP MOTIF.
                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 SPDRCKCKK-VKPTLATYLSKNYSYVIHAKIKAVQRSGC 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   186 GPFVCKCREPFVPIL----KESHPLYNKVRTGQVPNC 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9EQDO: 008975;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Frizzled 5 precursor (Frizzled-5) (Fz-5) (mFz5).
                                                                                                                                                                                                                                                                                                                                             ; Pred, No. 8,4e-21
37; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     577 AA.
                               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                  18.0%; Score 338.5;
                                                                                                                                                                                                                   PDZ-BINDING
                                                                                                                                                                                                                                                                                                             64551 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/6N; TISSUE-Gut;
PubMed-11092808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Development 128:25-33(2001).
[2]
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                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                    1449
5500
5521
585
585
585
47
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151
262
345
357
402
585 AA;
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      Local S.
73;
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                                                       TRANSMEM
DOMAIN
                                                                                                                                                                                                                                          CARBOHYD
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CONFLICT
CONFLICT
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                                 RANSMEM
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Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P.,
A large family of putative transmembrane receptors homologous to the
A large family of putative transmembrane receptors homologous to the
Product of the Drosophila tissue polarity gene frizzled.";
The product of the Drosophila tissue polarity gene frizzled.";
J. Biol. Chem. 271:4468-4476(1996).

I. FUNKTION: Receptor for Wht proteins. Most of frizzled.";
The accoupled to the beta-catenin canonical signaling pathway, which ladds to the activation of dishevelled proteins, inhibition of GSK-3 Kinase, nuclear accumulation of beta-catenin and activation of GSK-3 Kinase, nuclear accumulation of beta-catenin and activation of GSK-3 Kinase, nuclear accumulation of beta-catenin and activation of calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 Kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and interrecellular transmission of polarity information during tissue morphogenesis and in placental contractions. Was a roll in yolk sac anglogenesis and in placental contractions. Wascularization. Binds to Wnt2, Wnt10B, Wnt5A, but not to Wnt2B or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  colon.

DEVELOPMENTAL STAGE: Expressed in the yolk sac, placenta, eye and lung bud at 9.5 days post coitum (dpc). At 10.5 dpc, also expressed in the placental blood vessel of embryonic origin. DOWAIN: The fz domain is involved in binding with Wnt ligands (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Expressed in eye, kidney, lung, chondrocytes, epithelial cells of the small intestine and gobelet cells of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SRUGUC,
PROSITE; PS50038; FZ; 1.
PROSITE; PS50038; G_PROTEIN_RECEP_F2_4; 1.
Multigene family; G-protein coupled receptor; Transmembrane;
Multigene family; G-protein; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
FRIZILED 5.
EXTRACELLULAR (POTENTIAL).
1 (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
4 (POTENTIAL).
CYPOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                        Johnson M.A., Greenberg N.M.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF272146; AAG39355.1; -.
EMBL; AF005203; AAC01953.1; -.
MGD; MGI:108571; Fzd5.
InterPro; IPR0000539; Frizzled.
InterPro; IPR000024; Fz_domain.
InterPro; IPR000832; GPCR_secretin.
                                                                                                                      MEDLINE-96224032; PubMed-8626800;
                       STRAIN-C57BL/6; TISSUE-Prostate;
  SEQUENCE OF 207-296 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF01392; Fz; 1.
Pfam; PF01534; Frizzled; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00489; FRIZZLED. SMART; SM00063; FRI; 1.
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234
2234
2265
2267
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                                                                                                     SPECIFICITY.
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Adams M.D., Celliker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Hilp P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Woortman J.K., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Man K.H., Doyle C., Batter E.G., Helt G., Nelson C.R., Milklos G.L.G.,
A Abril J.F., Agbayani A., An Hi.-J., Andrews Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Berman B.P., Bhanddari D., Boslakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Ade Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
R. Posler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Allodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                          ä
                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophildae; Drosophila.
                                                                                                                                                                                                                                                          5 ILVALCLWLHLALGVRGAP-CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEE 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND BINDING TO WINGLESS THROUGH FZ DOMAIN. MEDLINE-96353971; Pubmed-8717036; Babnot P., Brink M., Samos C.H., Hsleh J.C., Wang Y., Macke J.P., Andrew D., Nathans J., Nusse R., Andrew D., Nathans J., Nusse R., Andrew D., Nathans J., Reland family from Drosophila functions as
                                                                                                                            N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
F6877C9B535CB865 CRC64;
                                                                                                                                                                                          Length 577;
                                                                                                                                                                                                                              41; Indels
                                               EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
                                                                 7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PR22_DROME STANDARD; PRT; 694 AA.
099VX3; 094016;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Frizzled protein 2 precursor (Frizzled-2) (Bf22)
F22 OR CG9739.
                                                                                                                                                                                            DB 1;
                                                                                                                                                                                              Score 331; DB 1;
Pred. No. 3.5e-20;
                                                                                                                                                                                                                          27; Mismatches
                                 6 (POTENTIAL)
                                                                                                               PDZ-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Berkeley;
MEDLINE-20196006; Pubmed-10731132;
ADDLINE-20196006; Pubmed-10731132;
                                                                                                                                                              63794 MW;
                                                                                                                                                                                              17.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wingless receptor.";
Nature 382:225-230(1996).
                                                                                                                                                                                                             Similarity 44.9957; Conservative
                                466
4495
516
577
1150
577
47
399
420
4646
467
4967
517
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577 AA;
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               DOMAIN
TRANSMEM
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CARBOHYD
                                               DOMAIN
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Refined D. Fenderon K.A. Farren G. H. Fez. Z., Kenlson JA. Ketchum K.A.

M. Kimmell B. E., Karlens G. H. Fez. Z., Kenlson JA. Ketchum K.A.

M. Kimmell B. E., Keller C. D. Kerlic C., Kreitz S. Xing D. L. Laiz Z.,

M. Lako, Y., Lel Y., Lel Y., Lel Y., Li J., Li Z., Liang Y., Lin X.,

Lako, Y., Lel Y., Lel Y., Lel Y., Kerlic C., Kreitz S. Xing D. L. Laiz Z.,

M. Merklor G., Milshina N.V., Kobarry C., Morris J., Woshiedi A.,

M. Merklor G., Milshina N.V., Kobarry C., Morris J., Woshiedi A.,

M. Merklor G., Milshina N.V., Kobarry C., Morris J., Woshiedi A.,

M. Merklor G., Milshina N.V., Kobarry C., Morris J., Woshiedi A.,

M. Mang G.Y., Merklow R. A., Wilson K., Milshina N.V., Kobarry C., Morris J., Woshiedi P.,

M. Miller E., Spendington K. S., Saunders E., Wang A., San Lh. T.,

M. Sylick B., Mang C., Trumer E., Wang R., San E.,

M. Miller S. M., Woodege T., Worley K., Wang S., San D.,

M. Miller S. M., Woodege T., Worley K., Wang S., Man J.,

M. Miller S. M., Woodege T., Worley K., Wang S., Man J.,

M. Miller S. M., Woodege T., Worley K., Wang S., Man J.,

M. Miller S. M., Woodege T., Worley K., Wang S., Man J.,

M. Miller S. M., Woodege T., Worley K., Wang S., Man J.,

M. Miller S. M., Woodege T., Worley K., Wang S., Man J.,

M. M. Mang S. W., Woodege T., Wooley K., Wang S., Man J.,

M. M. Mang S. W., Woodege T., Wooley K., Wang S., Man J.,

M. M. Hiller S. M., Woodege T., Wooley K., Wang S., Man J.,

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M. M. Larges General A. Recommon of the Merkler Linger General M., Mang M.,

M. M. Larges General A. Recommon of the Merkler S., Man S., Man S., Man M.,

M. M. Larges General A. Recommon of the Merkler S., Man S., Man M., Mang M.,

M. M. Larges G., Man M., Man M., Man M., Man M., Mang M.,

M. M., Mang M., Man M., M., Man M., Man M., Man M., Man M., M., Man M., M., M., M., M., M
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binds wingless protein and is in the Williams syndrome deletion at
                                                                                                                                                                                                                                                                                                                                                                                                                                          84 ICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESLACDELPVYDRGVCISPEAIV 143
                                                                                                                                                                                                                                                                                                                                                                              24 CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEELVDVNCSAVLRFFFCAMYAP 83*
                                                                                                                                                                                                                                                                                                                                                      37; Indels 24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutaleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
V -> A (IN REF. 1).
S -> T (IN REF. 1).
6C510F13CBAFB096 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Fetal brain;
MEDLINE-97227293; PubMed-9147651;
Wang Y.-K., Samos H.C., Peoples R., Perez-Jurado L.A., Nusse R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Oesophageal carcinoma;
MEDILINE-98374323, PubMed-9707618,
Tanaka S., Aklyoshi T., Mori M., Wands J.R., Sugimachi K.;
"A novel frizzled gene identified in human esophageal carcinoma
                                                                                                                                                                                                                                                                                                                             Length 694;
                                                                                3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Frizzled 9 precursor (Frizzled-9) (Fz-9) (Fz-66).
                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
           FRIZZLED PROTEIN 2.
EXTRACELLULAR (POTENTIAL).
                                                        2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                   1 (POTENTIAL).
CYTOPLASMIC (POFENTIAL).
                                                                                                                                                                                                                               LYS-THR-X-X-X-TRP MOTIF, PDZ-BINDING.
                                                                                                                                                                                                                                                                                                                           16.9%; Score 318; DB 1; 39.4%; Pred. No. 5.4e-19; iive 25; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              591 AA.
                                                                                                                                                                                                         GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hum. Mol. Genet. 6:465-472(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144 TDLPEDVKWIDITPDMMVQERP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75451 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 269-329 FROM N.A.
                                                                                                                                                                                                                                                                                                                              Query Match 16.9%
Best Local Similarity 39.4%
Matches 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo saplens (Human).
                                                                                                                   461
5035
535
535
556
606
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608
78
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417
417
417
44, AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FZD9 OR FZD3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FZD9_HUMAN
                                                                                                                                            DOMAIN
TRANSMEM
                                                                                                                                                                   DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                     CARBOHYD
                                   RANSMEM
                                                           RANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       000144;
                      DOMAIN
                                              DOMAIN
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                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                    124
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                                                                                                                                                                                                                                 SITE
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200
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                 Proc. Natl. Acad. Sci. U.S. 95:10164-10169(1998).

-:- FUNCTION: Receptor for Wht proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Whnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Whr.mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated
                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: Integral membrane protein. Localizes in the plasma membrane (By similarity).

Plasma membrane (By similarity).

TISSUE SPECIFICITY: Expressed predominantly in adult and fetal brain, testis, eye, skeletal muscle and kidney. Moderately expressed in pancreas, thyroid, adrenal cortex, small intestine and stomach. Detected in fetal liver and kidney.

DOMAIN: Lys-Thr-X-X-Trp motif is involved in the activation of the Wart/Deta catenin signaling pathway (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
-:- CAUTION: Has been first described as FZD3 in litterature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PSS0038; Fz; 1. PROSITE; PSS0261; G_PROTEIN_RECEP_F2_4; 1. Multigene family; G-protein coupled receptor; Transmembrane; Developmental protein; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRIZZLED 9.
EXTRACELLULAR (POTENTIAL).
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3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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6 (POTENTIAL).
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Interpro; IPR00004; Fz_domain.
Interpro; IPR000832; GPCR_secretin.
Pfam; PF01392; Fz; 1.
Pfam; PF0134; Frizzled; 1.
PRINTS; PR00489; FRIZZLED.
SMART; SM00063; FRI; 1.
mediates APC/beta-catenin signals.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U82169; AAC51174.1; -.
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MIM; 601766;
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FIGURE STATES ST
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STRAIN-CS-FRUNGARY STATESUB-Embryonic head;

X Kawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Riejschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kuchil P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fuljita M., Gariboldi M.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

Kordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

Sazaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Stoch K.-F.,

Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Brownstein M., Barshave V., Kawaji H., Kohtsuki S.,

Brownstein M., Barshave V., Kawaji H., Kohtsuki S.,

Brownstein M., Brown M., Hansegawa Y., Kawaji H., Kohtsuki S.,

Brown M., Brown M., Rodriguez C., Willming L.,

Brown M., Brown M., Rodriguez C., Willming L.,

Brown M., Rodriguez C., Wallming D.,

Brown W., Rodriguez C., Wallming D.,

Brown W., Rodriguez C., Willming D.,

Brown W., Rodriguez C., Wallming D.,

Brown W., Rodriguez C., Willming D.,

Brown W.,

Brown W., Rodriguez C., Willming D.,

Brown W.,

Brown W., Rodriguez C., William W.,

Brown W.,

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Van Raay T.J., Rasmussen J.T., Rao M.S.;
"A novel mouse frizzled gene expressed in early neural development.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                             69 AAABLAEFAPLVQYGCHSHLRFFLCSLYAPMCT-DQVSTPIPACRPMCEQARLRCAPIME 127
                                                                                                                                                                                                                                                                               54 AILAIEQYEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMK 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.
STRAIN=129/SvJ; TISSUE-Brain;
MEDIINE-99216417; Pubmed=10198163;
Wang Y.-K., Spoerle R., Paperna T., Schughart K., Francke U.;
"Characterization and expression pattern of the frizzled Gene Fzd9,"
the mouse homolog of FZD9 which is deleted in Williams-Beuren
                                                                                                                Gaps
                                                                                                                                                                                               8 ALCLWLHLALG------VRG---APCEAVRIPMCRHMPWNITRMPNHLHHSTQEN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                             20;
                                                        Length 591;
                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PZD9_MOUSE STANDARD; PRT; 592 AA. Q9R216; Q9CX16; 035494; Q9R218; 15-JUN-2002 (Rel. 41, Created) 115-JUN-2002 (Rel. 41, Last sequence update) 115-JUN-2002 (Rel. 41, Last annotation update) Frizzled 9 precursor (Frizzled-9) (F2-9) (MF23). FZD9 OR FZD3.
0D3784A78DF0B2E5 CRC64;
                                                  16.6%; Score 312; DB 1;
llarity 40.4%; Pred. No. 1.4e-18;
Conservative 27; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                               114 MYNHSWPESLACDELPVYDRGVCISPEAIVTDLPED 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 QFNFGWPDSLDCARLPTRN-----DPHALCMEAPEN 158
64466 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Mouse)
591 AA;
                                                                            Local Similarity
es 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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SEQUENCE
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Calo L., Mimmack M.L., Keverne E.B., Emson P.C.;

"Localization of the mouse frizzled gene mF2D3 in the olfactory
repithelium and in the vomeronasal organ.";

"Explaint and in the vomeronasal organ.";

"Explaint and in the vomeronasal organ.";

"In submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

"In submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

"In FUNCTION: Receptor for Wnt proteins. Most of frizzled receptors

are coupled to the beta-catenin canonical signaling pathway, which
leads to the activation of dishvelled proteins, inhibition of

"SK-3 kinase, nuclear accumulation of beta-catenin and activation

of Wnt target genes. A second signaling pathway involving PKC and

colcium fluxes has been seen for some family members, but it is

not yet clear if it represents a distinct pathway or if it can be

integrated in the canonical pathway, as PKC seems to be required

to involve interactions with G-proteins. May be involved in

transduction and intercellular transmission of polarity

information during tissue morphogenesis and/or in differentiated
                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
CAUTION: Has been first described as F2D3 in litterature.
                                                                                                                                                                                                           plasma membrane.
TISSUE SPECIFICITY: In the embryo, found in the neural tube, trunk
                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein. Localizes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity).
SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRIZZLED 9.
EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF035205, MINESTELL, Y17709; CAB44237.1; -. RWB.; MGD; MG1:1313278; Fzd9. InterPro; IPR000539; Frizzled. InterPro; IPR000024; Fz_domain. InterPro; IPR000833; GPCR_secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF088850; AAD27789.1; -. EMBL, AK021164; BAB32311.1; -. EMBL, AF033585; AAB87503.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01392; Fz; 2.
Pfam; PF01534; Frizzled; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0489; "RIZZLED. SMART; SMO0063; FHI; 1.
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54 AILAIEQYEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMK 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 ALCLWLHLALG-----VRG---APCEAVRIPMCRHMPWNITRMPNHLHHSTQEN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 ALLLWOLLATGGAALEIGRFDPERGRGPAPCQAMEIPMCRGIGYNLTRMPNLLGHTSQGE 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wheeler G.N., Hoppler S.; "Two novel Xenopus frizzled genes expressed in developing heart and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
S -> P (IN REF. 3).
OL -> HC (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 592;
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               2 (POTENTIAL)
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                            3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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E -> S (IN REF. 4)
E -> D (IN REF. 4)
C -> D (IN REF. 3)
C -> D (IN REF. 3)
L -> P (IN REF. 2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.5%; Score 310; 39.7%; Pred. No. 2
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Medina A., Reintsch W., Steinbeisser H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
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MEDLINE-99376692; Pubmed-10446283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64994 MW;
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-!- SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
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549 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      through cleavage stages. Levels rise through gastrula (localized to the presumptive neuroectoderm and deep cells of the involuting mesoderm) and neurula stages (localized to the neural folds in presumptive neural-crest-cell-derived areas), peaking at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Wnt/Deta-catenin signaling pathway (By similarity). DOMAIN: The fz domain is involved in binding with Wnt ligands (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arches and pronephros). DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of
                                                                                                                                                                                                                                                             Sumanas S., Strege P., Heasman J., Ekker S.C.;
"The putative Wnt receptor Xenopus frizzled-7 functions upstream of beta-catenin in vertebrate dorso-ventral mesoderm patterning.";
Development 127:1981-1990(2000).
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND COUPLING TO BETA-CATENIN PATHWAY.
MEDLINE-20424135; PubMed-10969734;
MEDLINE-20424135; PubMed-10969734;
MEDLINE-20424135; PubMed-10969734;
MEDLINE-20424135; PubMed-10969794;
MEDLINE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAY MITSA. According to Ref.3: binds to Whili.
TISSUE SPECIFICITY: In the embryo, expressed in the heart, pronephros and otic vesicles.
DEVELOPMENTAL STAGE: Present in unfertilized eggs, persisting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tailbud stage (detected in the eye, heart regions, pharyngeal
*Xenopus frizzled 7 can act in canonical and non-canonical Wnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
                                                                                                                              Djiane A., Riou J.-F., Umbhauer M., Boucaut J.-C., Shi D.-L., "Role of frizzled 7 in the regulation of convergent extension movements during gastrulation in Xenopus laevis.";
                 signaling pathways: implications on early patterning and
                                                                                                                                                                                                                SEQUENCE FROM N.A., AND COUPLING TO BETA-CATENIN PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gradl D., Buhrmann V., Wedlich D.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Dev. Growth Differ. 42:347-357(2000).
                                                                                                                                                                                                                                TISSUE-Occyte;
MEDLINE-20214855; PubMed-10751186;
                                                                                                 TISSUE-Embryo;
MEDLINE-20323171; PubMed-10862746;
                                                                                                                                                                                Development 127:3091-3100(2000).
                                               Dev. 92:227-237(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                SEQUENCE FROM N.A.
                                  morphogenesis."
                                                                                                                                                                                                                                                                                                                                                                                                                                   manner
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RECEPTORS.

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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50038; FRI; 1.
PROSITE; PS50038; FZ; 1.
PROSITE; PS50261; G_PROFEIN_RECEP_FZ_4; 1.
Multigene family; G_Protein coupled receptor; Transmembrane; Developmental protein; Glycoprotein; Signal.
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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C -> G (IN REF. 2).
SPYL -> TLNP (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C -> G (IN REF. 1.)
S -> A (IN REF. 1.)
T -> I (IN REF. 6.)
S -> F (IN REF. 6.)
I -> L (IN REF. 1.)
Q -> H (IN REF. 1.)
Q -> G (IN REF. 1.)
S -> G (IN REF. 1.)
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                                                                                                                                                                                                                                                                                                                                     EMBL, AF039215, AAF63152.1; -. InterPro; IPR000039; Frizzled. InterPro; IPR000024; Fz. domain. InterPro; IPR000032; GPCR_secretin. Pfan; PF01534; Frizzled; 2. Pfan; PF01534; Frizzled; 2. PRINTS: PR00489; FRIZZLED.
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                                                                                                                                                                                                                                                             EMBL; AF179213; AAD52671.1; -. EMBL; AJ243323; CAB45875.1; -. EMBL; AF114151; AAD21247.1; -.
                                                                                                                                                                                                                                     EMBL; AF159106; AAD44331.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Amat target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated
DOMAIN: Lys.Thr.X.X.Trp motif is involved in the activation of
the Wnt/Deta-catenin signaling pathway (By similarity).
DOMAIN: The fz domain is involved in binding with Wnt ligands (By
                                        115 YNHSWPESLACDELPVYDRG-VCI-----SPEAIVTD----LPEDVKWIDITPDMMVQ 162
                                                                     126 FGFOWPERLRCENFPVHGAGEICVGONTSDNSPSGPTARPSPYLPDSITF-----0 176
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-21192958; PubMed-11295046;
Saltoh T., Hiral M., Katoh M.;
"Molecular cloning and characterization of human Frizzled-8 gene on chromosome 10pl1.2";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Most abundant in fetal kidney, followed by brain and lung. In adult tissues, expressed in kidney, heart,
                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Frizzled 8 precursor (Frizzled-8) (Fz-8) (hF28).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 1 FRIZZLED (F2) DOMAIN.
                                                                                                                                                                                                     694 AA
                                                                                                                   177 PHPHRDFTCPRQ-----LKVPPYLA 196
                                                                                                  163 ERP-LDVDCKRLSPDRCKCKKVKPTLA 188
                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             pancreas and skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Int. J. Oncol. 18:991-996(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AB043703; BAB41064.1; -. EMBL; AL121749; CAC10185.1; -.
                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HGNC:4046; FZD8
                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew; HGNC:4040
MIM; 606146; -.
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                                                                                                                                                                                                   FZD8_HUMAN
Q9H461;
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59 EQYEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 SILVALCLWLHLALGVRGA-----PCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID*10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                       PROSITE; PS50038; F2, 1.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
Multigene family, G=protein coupled receptor; Transmembrane;
Developmental protein; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 694;
                                                                                                                                                                                                                                                    1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FZD1_MOUSE STANDARD; PRT; 642 AA. 070421; 008974; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Frizzled 1 precursor (Frizzled-1) (FZ-1) (mFz1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.4%; Score 308; DB 1; 40.1%; Pred. No. 3.7e-18;
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30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        5 (POTENTIAL)
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N-LINKED
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POLY-PRO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 WPESLACDELPVYDRGVCISPEAIVTD 145
                 InterPro; IPR000024; Fz_domain.
InterPro; IPR000832; GPCR_secretin.
Pfam; PF01192; Fz; 1.
Pfam; PF01534; Frizzled; 1.
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STRAIN-C57BL/6; TISSUE-Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73300 MW;
InterPro; IPR000539; Frizzled
                                                                                      PRINTS; PRO0489; FRIZZLED.
SMART; SM00063; FRI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 40.1 es 59; Conservative
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TRANSMEM
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Matches
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Johnson M.A., Greenberg N.M.;
Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

Le Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.

The Coupled to the Deta-catenin canonical signaling pathway, which lads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of wit target genes. A second signaling pathway involving FKC and calcium fluxes has been for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN: The fz domain is involved in binding with Wnt ligands (By similarity).
                                                                                                                                                                                                                                                                                                                                                           -:- TISSUE SPECIFICITY: Expressed in chondrocytes.
-:- DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of
the Wnt/Deta-catenin signaling pathway (By similarity).
              tu L., Tan L., Goldring M.B., Olsen B.R., Li Y.;
Expression of frizzled genes in mouse costochondral chondrocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMAK1; SMVVVV...
PROSTTE: PS50038; FZ; 1.
PROSTTE: PS50038; FZ; 1.
Multigene family: G-protein coupled receptor; Transmembrane;
Multigene family: G-protein; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1196625; Fzdl.
InterPro; IPR000539; Frizzled.
InterPro; IPR00024; Fz_domain.
InterPro; IPR000832; GPCR_secretin.
 MEDLINE-21233588; Pubmed-11334716;
                                               Matrix Biol. 20:147-151(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF054623; AAC12873.2; -. EMBL; AF005202; AAC01952.1; -.
                                                                          SEQUENCE OF 302-376 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01392; Fz; 1.
Pfam; PF01534; Frizzled; 2.
PRINTS; PR00489; FRIZZLED.
SMART; SM00063; FRI; 1.
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349
349
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485
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594
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TRANSMEM
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Mech. Dev. 93:195-200(2000).

Nech. Dev. 93:195-200(2000).

I FUNCTION: Receptor for Mut proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSR-3 kinase, nuclear accumulation of beta-catenin and activation of Wh target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated inactivation of GSR-3 kinase. Both pathways seem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Expressed broadly in cranial ectoderm. Also
expressed in the developing somites and in other cranial placodes,
including the olfactory, lens, otic placodes (lateral half of the
vesicle) and epibranchial placodes. Low level of expression in all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                            56 LLLWLLEAPLLLGVRAQAAGQVSGPGQQAPPPPQPQQSGQQYNGERGISIPDHGYCQPIS 115
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Information during tissue morphogenesis and/or in differentiated
                                                                                                                                                                                                                                                                            29 IPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEELVDVNCSAVLRFFFCAMYAPICTLE
                                 N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
P -> R (IN REF. 2).
S -> F (IN REF. 2).
OAADOCODC820BGCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to involve interactions with G-proteins. May be involved in
                                                                                                                                                                        43;
                                                                                                                                       DB 1; Length 642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIINE=20245319; PubMed=10781956;
Stark M.R., Biggs J.J., Schoenwolf G.C., Rao M.S.;
"Characterization of avian frizzled genes in cranial placode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kengaku M., Twombly V., Tabin C.;
"Expression of Wnt and Frizzled genes during chick limb bud
                                                                                                                                                                                                                                                                                                                                                                 transduction and intercellular transmission of polarity
                                                                                                                                                                                                                                                                                                                                                89 FLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESLACDELPVYDRG-VCI 137
                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cold Spring Harb. Symp. Quant. Biol. 62:421-429(1997).
   LYS-THR-X-X-X-TRP MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FZD7_CHICK STANDARD; PRT; 567 AA. 057329; Q9IA04; D15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Frizzled 7 precursor (Frizzled-7) (F2-7) (CF2-7).
                                                                                                                                                                        36
                                                                                                                                     Score 307.5; DB 1
Pred. No. 3.7e-18;
                                                                                                                                                                        24; Mismatches
                                                                                                                                                                                                          9 LCLWL---HLALGVRG------AP-----
                   PDZ-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Limb bud;
MEDLINE=98260739; PubMed=9598377;
625 LY
642 PT
125 N-
226 N-
341 P
351 P
                                                                                                                                     16.48;
                                                                                                                                                                        Conservative
 620
640
125
226
341
352
642 AA;
                                                                                                                                                        Similarity
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'n

Pred. No. 4.2e-18;

39.28;

Best Local Similarity

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           or DEVELOPMENTAL STAGE: First detected as stage 6 in the forming neural tube and somites, but not in trunk surface ectoderm. By stage 8, expression persists in the cranial ectoderm and is upregulated in the presomptive olfactory placodes. By stages 11-12, expression declines in the neural tube, but not in the cranial ectoderm; in somites, expressed all along the rostral-caudal axis as well as in presegmental mesenchyme caudal to the developing somites. Lens and otto placode expression first visible at stage 12, strongest at stages 13-16. Detected uniformly in ectoderm and mesenchyme of the limb primordia at stage 17. By stage 18, decrease of ectodermal, otic, lens and olfactory placode expression; expression; expression appears in the most distal mesoderm of the autoped, in the ventricular zone of the neural tube from the
                                                                                                                                                                                                                                                                                            the Wnt/beta-catenin signaling pathway (By similarity). DOMAIN: The fz domain is involved in binding with Wnt ligands (By
                                                                                                                                                                                                                                                                           DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of
                                                                                                                                                                                                                                            forebrain to the spinal cord, in the dermomyotomes and the tail
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
HE -> QD (IN REF. 2).
                                                                                                                                                                                                                                                                                                                        similarity).
SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHAKT; SHUNCOL, PEROTEIN, RECEP_F2_4; 1. PROSITE; PS50261; 0_PROTEIN, RECEP_F2_4; 1. Multigene family; G-protein coupled receptor; Transmembrane; Developmental protein; Glycoprotein; Signal. POTENTIAL.
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3EFF0381FC899BC3 CRC64;
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 FRIZZLED (FZ) DOMAIN.
 mesoderm derivatives in the limb buds.
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InterPro; IPR000024; Fz_domain.
InterPro; IPR000832; GPCR_secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF031831; AABB7969.1; -. EMBL; AF224317; AAF61097.1; -.
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Pfam; PF01534; Frizzled; 1.
PRINTS; PR00489; FRIZZLED.
SMART; SM00063; FRI; 1.
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567 AA;
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TRANSMEM
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CARBOHYD
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DB 1; Length 567;

Score 306;

16.3%;

Query Match

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Trizziero is expressed in the spendant organizer and plays a fore in bevelopment 125:2687-2700(1998).

Development 125:2687-2700(1998).

I pevelopment 125:2687-2700(1998).

The coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSK-3 kinase, nuclear accumulation of beta-catenin and activation of Mnt target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wnt-mediated lnactivation of GSK-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and interacellular transmission of polarity information during tissue morphogenesis and/or in differentiated tissues. Activation by Wnt8, Wnt5A or Wnt3A induces expression of beta-catenin target genes. Displays an axis-inducing activity.

SUBCELLUIAR LOCATION: Integral membrane protein.

The Spenann organizer prior to involutein of the dorsal blastopore blastula stages. At early gastrula, expressed in the deep cells of graced in preceds. Becomes restricted to the anterior ectoderm by the end of gastulalian. At neurula stages, localized in the most anterior region of the embryo, mainly in the anterior ectoderm including telencephalic and cement gland regions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deardorff M.A., Tan C., Conrad L.J., Klein P.S.; *Frizzled-8 is expressed in the Spemann organizer and plays a role in
                                                                                                                               51 QENAILAIEQYEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEP 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Wht/beta-catenin signaling pathway (By similarity).
                                                                                                                                                        12 WLHLA---LGVRGAPCEA-------VRIPMCRHMPWNITRMPNHLHHST 50
                                                                                   14 WLGLAALLAALLGTPCAAAHHEDKAISVPDHGFCQPISIPLCTDIAYNQTILPNLLGHTN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity).
SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND COUPLING TO BETA-CATENIN PATHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Itoh K., Jacob J., Sokol S.Y.;
"A role for Xenopus Frizzled 8 in dorsal development.";
Mech. Dev. 74:145-157(1998).
                                                                                                                                                                                                                                                                                                                                                                           FZD8_XENLA STANDARD; PRT; 581 AA. 093274; 09Y155; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Frizzled 8 precursor (Frizzled-8) (Fz-8) (Xfz8).
                                                                                                                                                                                                                       111 LMKMYNHSWPESLACDELPVYDRG-VCISPEAIVTDLP 147
                                                                                                                                                                                                                                                23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98301424; PubMed-9636083;
62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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FZD8_XENLA
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65 FWPLVVIHCSPDLKFFLCSMYTPIC-LEDYKKPLPPCRSVCERARAGCAPLMROYGFAWP 123
                                    ESLACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERP----LDVDCKRLSPD 176
                                                 :: || || :: | : | : | : | : | 124 DRMRCDRLP--EQG---NPDTLCMDYYNRTEQTTAAPSHPEPPRPPARSVPKGRTRVEPP 178
                                                                              177 R-----CKCKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFK 225
                                                                                                    179 RSRSRATGCESGCQCR--APMVQV---SNERHPLYNRVRTGQ-
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                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bicinformatics and the EMBL outstation the European Bicinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 YEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LSILVALCLWLH--LALGVRCAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
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N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                        PROSITE; PS50038; FZ; 1.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
Multigene family; G-protein coupled receptor; Transmembrane;
Developmental protein; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 581;
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EXTRACELLULAR (POTENTIAL).
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1 (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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           SIMILARITY: CONTAINS 1 FRIZZLED (F2) DOMAIN.
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-> V (IN REF. 2)
-> G (IN REF. 2)
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CYTOPLASMIC (F
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                                                                                                                                                                                                                                                                                 FRIZZLED 8
                                                                                                                                                                                                                                                                      POTENTIAL.
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                                                                                                                                                        InterPro; IPR000024; Fz_domain.
InterPro; IPR000832; GPCR_secretin.
Pfam, PF01534; Frizzled; 2.
Pfam, PF01534; Frizzled; 2.
PRINTS; PR00489; FRIZZLED.
SMART; SM00063; FRI; 1.
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                                                                                                                        EMBL; AF017177; AAC31121.1; -.
                                                                                                                                 EMBL; AF033110; AAC77361.1; -. InterPro; IPR000539; Frizzled.
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239
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Local Sim.
79;
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Wech. 93:195-200(2000).

-1- FUNCTION: Receptor for Wht proteins. Most of frizzled receptors are coupled to the beta-catenin canonical signaling pathway, which leads to the activation of dishevelled proteins, inhibition of GSR-3 kinase, nuclear accumulation of beta-catenin and activation of Wht target genes. A second signaling pathway involving PKC and calcium fluxes has been seen for some family members, but it is not yet clear if it represents a distinct pathway or if it can be integrated in the canonical pathway, as PKC seems to be required for Wht-mediated inactivation of GSR-3 kinase. Both pathways seem to involve interactions with G-proteins. May be involved in transduction and intercellular transmission of polarity information during tissue morphogenesis and/or in differentiated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            In the developing somities (dermomyotome).

DEVELOPMENTAL STAGE: Somites and placodal expression appears at stage 9. At this stage, more obvious expression is detected in the neural tube (midbrain and rostral hindbrain), and persists through about stage 15. Strongly expressed in the ectoderm and around the expression is tagge 12. At stage 16, other expression declines, expression in epibranchial placodes begins and peaks at stage 20. Expression in the lens of the eye is first seen at about stage 15,
226 SSSPIPRTQVPLITNSSCQCPHILPHQDVL-----IMCYEWRSRMMLLENCLVEKW 276
                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: Expressed in the lens, otic placode (medial
wall of the vesicle) and in epibranchial placode. Also expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 307-592 FROM N.A. MEDINE-2024513; PubMed-1079156; MEDINE-2024513; PubMed-1079156; Stark M.R., Biggs J.J., Schoenwolf G.C., Rao M.S.; "Characterization of avian frizzled genes in cranial placode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98260739; PubMed-9598377;
Kengaku M., Twombly V., Tabin C.;
"Expression of wnt and frizzled genes during chick limb bud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cold Spring Harb. Symp. Quant. Biol. 62:421-429(1997).
                                                                                                                                                                                                                                                        FZD1_CHICK STANDARD; PRT; 592 AA. 057328; 091A07; 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Frizzled 1 precursor (Frizzled-1) (Fz-1) (cFz-1).
                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                         1 : : | |
264 RFKYPERPI 272
                                                                                            277 RDQLSKRSI 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Limb bud;
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g Q

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more evident at stage 16. At stage 17, seen in the ectoderm and mesenchyme of the limb primordia. Detected at stage 20 in the lip of the optic cup, in the mesenchyme surrounding the eye, in the ectoderm overlying the lens and in the ectoderm caudal and ventral of the olfactory placedes. From stages 20-30, expressed in cartilage and in the dermomyotomes and migrating sclerotomal cells
                                                                                                                                                                                                                                 the Wnt/Deta-catenin signaling pathway (By similarity).
DOMAIN: The fz domain is involved in binding with Wnt ligands (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 SAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESLACDELP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                         DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 ALGVRGAP-----CEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEELVDVNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
933876050cA6109D CRC64;
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6
                                                                                                                                                                                                                                                                                                similarity).
SIMILARITY: BELONGS TO FAMILY F2/SMO OF G-PROTEIN COUPLED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50038; FZ; 1.
PROSITE; PS50261; G_PROTEIN_RECEP_FZ_4; 1.
Multigene family; G_protein coupled receptor; Transmembrane; Developmental protein; Glycoprotein; Signal.
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4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EMBL; AF24314; AAF61094.1; -.
Interpro; IPR000039; Frizzled.
Interpro; IPR000024; Fz. domain.
Interpro; IPR000832; GPCR_secretin.
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Pfam; PF01534; Frizzled; 2.
PRINTS; PR00489; FRIZZLED.
SMART; SM00063; FRI; 1.
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                                                                                                                                                                                                        MEDLINE-96224032; PubMed-8626800; Wang Y., Macke J.P., Abella B.S., Andreasson K., Worley P., Gilbert D.J., Copeland N.G., Jenkins N.A., Nathans J.; A large femily of putative transmembrane receptors homologous to the product of the Drosophila issue polarity gene frizzled."; J. Blol. Chem. 271:4468-4476(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the Wnt/beta-catenin signaling pathway (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- TISSUE SPECIFICITY: Expressed in chondrocytes.
-1- DOMAIN: Lys-Thr-X-X-X-Trp motif is involved in the activation of the Wit/beta-catenin signaling pathway (By similarity).
                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
-!- SIMILARITY: BELONGS TO FAMILY FZ/SMO OF G-PROTEIN COUPLED
                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Frizzled & precursor (Frizzled-8) (Fr-8) (MF28).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@lsb-sib.ch)
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InterPro; IPR000832; GPCR_secretin.
                           PRT;
                                                                                                                                                                                                                                                                                                             COUPLING TO BETA-CATENIN PATHWAY
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                           STANDARD;
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                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                target genes.
                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTORS
                           FZD8_MOUSE
                                       061091;
RESULT 15
FZD8_MOUSE
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Ouery Match 16.2%; Score 305; DB 1; Length 685;
Best Local SImilarity 39.5%; Pred. No. 6.4e-18;
Matches 58; Conservative 31; Mismatches 46; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 SILVALCLWLHLALGVRGA----PCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAI 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GICNAC. .) (POTENTIAL).
N-LINKED (GICNAC. .) (POTENTIAL).
N-LINKED (GICNAC. .) (POTENTIAL).
F333B49474411267 CRC64;
                 PROSITE; PS50038 FZ; 1.
PROSITE; PS50048; G_PROTEIN_RECEP_F2_4; 1.
Multigene family; G-protein coupled receptor; Transmembrane;
Developmental protein; Glycoprotein; Signal.
SIGNAL 1 27 POTENTAL.
                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

STANCELLULAR (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

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POLY-ALA.
POLY-GLY.
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9 9 9 Search completed: March 7, 2003, 11:24:18 Job time : 16 secs



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0921n6 mus musculu 091s5 rattus norv 03522 rattus norv 0924n2 rattus norv 091s4 rattus norv 091s4 rattus norv 091s9 gallus gall p7993 kenopus lae p7993 kenopus lae p7993 kenopus lae p7993 mus musculu 09ptd9 gallus gall 0957b oryctolagus 0951b1 oryctolagus 0951b1 oryctolagus
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                                                       March 7, 2003, 11:20:59; search time 35 Seconds (without alignments) 2036.923 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                    1 MFLSILVALCLWLHLALGVR......SPKKNIKTRSAQKRTNPKRV 346
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                                                                                                                                                                                            671580
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                      671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
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Listing first 45 summaries
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0921N6
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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        17
        318.5
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        0916V7
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        brachydanio

        18
        318.5
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        318.5
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        09YT7
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        312.5
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        14
        08TAN2
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        22
        303.5
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        09YT49
        09Btt3
        09Btt4
        09Btt4
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ALIGNMENTS

RESULT 014877	RESULT 1 014877			,						
日名	014877	PRELIMINARY;	ARY;	PRT;	346 AA.	Α.				
턴	01-JAN-1998 01-JIN-1998	(TrEMBLrel.	05,	Created) Last sequence update)	ence	update)				
15	01-DEC-2001	(TrEMBLrel.	19,	Last annotation update)	tatio	n update	(a)			
田で	FrpHE.									
၈ ဗ	Homo sapiens (Human). Eukarvota: Metazoa: Chordata: Craniata: Vertebrata:	(Human) Metazoa; (Chordata	Craniat	a: Ve	rtebrata	1; Euteleostomi;	tomi;		
ဗ္ဂ	Mammalia; Eutherla;	theria; 1	Primates;	Catarr	in1;	Hominida	Catarrhini; Hominidae; Homo.			
×	NCBI_TaxID=9606;	1909								
z :	[1]									
ž č	TISSUE-ENDOMETRIUM:	M N.A.								
Z.	Abu-Jawdeh G.M., Comella N., Brown L.F., Tognazzi K., Kocher	.M., Come	ella N.,	Brown L.	F., T	ognazzi	K., Kochei	0		
RŢ	"frizzled related protein frpHE (Homo Sapiens).";	lated pro	otein fr	энЕ (ношс	Sapi	ens).";				
RL	Submitted (N	(AR-1998)	to the 1	EMBL/GenE	3ank∕D	DBJ data	abases.			
25	EMBL; AF026692; AAC04617.1;	92; AACO	4617.1;							
O.R	InterPro; IPR000024; Fz_domain.	PR000024;	Fz_doma.	.u.						
D.R	InterPro; IPR001134;	PR001134;	Netrin_C.	,;						
2	Ptam; PF01392; Fz; 1.	12; FZ; 1	•							
2	Ptam; PF0175	9; NTR;	1.							
D.R.	SMART; SM00063; FRI; 1.	63; FRI;	1.							
S.	S	50038; FZ	. 1.		1					
Ö	SEQUENCE	346 AA;	39860 MW;		043E44	75D78D43E444CC2A CRC64;	RC64;			
Õ	Query Match		100.08;		1879;	Score 1879; DB 4;	Length 346;	.;		
m z	Best Local Similarity 100. Matches 346: Conservative	llarity Conserva	80	- :	No. 6.	7e-164;	Indels	0	Gaps	
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'n	111111							3 -		
Q	1 MFLSILV	ALCLWLHE	ALGVRGAP	EAVRIPM	RHMP	NITRMPN	MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ	LAIEO	09	
ργ	61 YEELVDV	NCSAVLRF	FFCAMYAP	СТЕБЕТН	PIKPC	KSVCORA	YEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCORARDDCEPLMKMYNHSWP	WHSW	120	
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301 KKOIASRTSRTSRSNPPKSKGRPPAPKPASPKKNIKARSAPKKSNLKK 348
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                                                                               181 KKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLITN 240
                                                                                                                                                                   SSCOCPHILPHODVLIMCYEWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chang J.T., Esumi N., Moore K., Li Y., Zhang S., Chew C., Goodman B., Rattner A., Moody S., Stetten G., Campochiaro P.A., Zack D.J.;
"Cloning and characterization of a secreted frizzled-related protein that is expressed by the retinal pigment epithelium.";
Hum. Mol. Genet. 0:0-0(1999).
BMBL; AFILTYO9; AAD12:06.1; -.
MGD; MGI:892010; SFIP4.
InterPro; IPR001034; Fz_domain.
InterPro; IPR001134; Netrin_C.
Pfam; PF01759; NTR; 1.
SMART; SM00063; FZ: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MLRSILVALCLWLRLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ
                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 11; Length 351;
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                                                                                                                                                                                                                                                   6CB0B625920A54FE CRC64;
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01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Secreted frizzled-related sequence protein 4.
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Pred, No. 9.2e-152;
9; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last seq 01-OCT-2001 (TrEMBLrel. 18, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40342 MW;
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92.5%;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 procesin frpAP.
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Ruttus norvegicus (Rat).
Rutasyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthoria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                           Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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"Transcriptional activity of the promoter region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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Pred. No. 1.9e-150;
8; Mismatches 18;
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EMBL; AF100346; AAF66480.1; -.
ILICEPPED; IPRO00024; F2_domain.
INCEPPED; IPRO01134; Netrin_C.
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                                              01-0CT-2000 (TrEMBLrel, 15, 01-0CT-2000 (TrEMBLrel, 15, 01-DEC-2001 (TrEMBLrel, 19, Frizzled related protein.
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Matches 319; Conservative
  PRELIMINARY;
                                                                                                                                                      Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                                                                                                                                                                                    related protein gene.";
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PROSITE; PS50038; FZ; 1
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Pfam; PF01759; NTR; 1.
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09JLS5
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Pfam; PF01759; NTR; 1.
PROSITE; PS50038; FZ;
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09JLS4;
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                               Wolf V., Artuso L., Dharmarajan A., Guo K., Bielke W., Friis R.R., "A frizzled related Gene is upregulated in Physiological Apoptosis.";
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                     ESLACDELPVYDRGVCISPEAIVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCKC 180
                                                                                                                                                                                                                                                                                                                                                                                                              241 SSCQCPHILPHQDVLIMCYEWRSRWMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 SSCOCPHILPXQDVLIMCYERRSRAMLLENCLVEKWRDQLSRRSTQWEERLQEQQRTTQD 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                           "Apoptosis associated Gene Expression in Corpus luteum of the Rat."; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.

EMBL; AF012891; Amb65431.1; InterPro; IPR000024; Fz_domain.

InterPro; IPR000134; Netrin_C.

Pfam; PF01392; Fz; 1.

Pfam; PF01759; NTR; 1.

PROSITE; PS50038; FZ; 1.
                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                       1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ
                                                                                                                                                                                                                                                                                                                    KKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLITN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 KKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSSSPIPRTQVPLITN
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                                                                                                                                                                                                                                                       91.5%: Score 1720; DB 11; Length 348; 92.2%; Pred. No. 2.4e-149; live 9; Mismatches 18; Indels 0
                                                                                                 Guo K., Wolf V., Dharmarajan A., Feng 2., Bielke W., Susanne Friis R.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
Chan K.W., Yam J.W.P., Hsiao W.W.L.;
Chan K.W., Yam J.W.P., Hsiao W.W.L.;
"Brain specific rat frizzled related protein gene.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF220608; AAK58311.1;
InterPro; IPR000024; Fz_domain.
InterPro; IPR001134; Netrin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39735 MW; 08BA5BF909AE7B64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 KKKTAGRTSRSNPPKPKGKPPAPKPASPKKNIKTRSAQKRTNPKR 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                    Best Local Similarity 92.2
Matches 318; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                    STRAIN-SPRAGUE-DAWLEY;
                                                                                          STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01392; Fz; 1.
                                                                                                                                                                                                                                     348 AA;
                                                                    [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                          Query Match
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Q924N2
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61 YEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWP 120
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C STRAIN=FISHER; TISSUE=LIVER;

X MEDLINE-21378144; PubMed-114485313;

X MEDLINE-21378144; PubMed-114485313;

Transcriptional activity of the promoter region of rat frizzled-
Transcriptional activity of the promoter region of rat frizzled-
Transcriptional activity of the promoter region of rat frizzled-
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Transcriptional activity of the promoter region of rate frizzled-
Transcriptional activity of the promoter region of rate frizzled-
Transcription
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                           Gaps
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                                                                                        Length 303;
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                                                                                                                                                                                      Indels
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8AB612A48933AAE1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                   79.0%; Score 1485; DB 11;
96.1%; Pred. No. 6.7e-128;
tive 2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1.8e-86;
1; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Frizzled related protein (Fragment)
34507 MW;
                                                                                                                                         Best Local Similarity 96.1
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 187; Conservative
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303 AA;
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us-09-909-775-2.rspt

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"Cloning and Expression of the Wnt Antagonists Sfrp-2 and Frzb during Chick Development.";
Dev. Biol. 218:183-198(2000).
EMBL, FAL18057; AMF225643.1; -.
InterPro; IPR000024; Fz_domain.
InterPro; IPR001134; Netrin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 CKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSS-SPIPHTQVPLI 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 LVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWPESL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 ACDELPVYDRGVCISPEAIVT----DLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCK 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 SILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEE 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97236496; PubMed=9118219; Wang S., Krinks M., Lin K., Luyten F.P., Moos M. Jr.; Wang S., Krinks M., Lin K., Luyten F.P., Moos M. Jr.; Fricks a secreted protein expressed in the Spemann organizer, binds and inhibits Wnt-8."; Cell 88:757-766(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                      239 TNSSCOCPHILPHODVLIMCY -- EWRSRMMLLENCLVEKWRDOLSKRSIQWEERLQEORR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachla; Anura; Mesobatrachla; Pipoldea; Pipidae;
NCBI_TaxID=8355;
                                                                                    Ladher R.K., Church V.L., Allen S., Robson L., Abdelfattah A.,
Brown N.A., Hattersley G., Rosen V., Luyten F.P., Dale L.,
                                                                                                                                                                                                                                                                                                                                                44.1%; Score 828; DB 13; Length 315; 50.0%; Pred. No. 9.9e-68;
                                                                                                                                                                                                                                                                                                                35003 MW; 6EBC58DB5335505D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 AA.
                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 50.0%; Pred. No. 9.9e-
Matches 162; Conservative 52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                   SEQUENCE FROM N.A. MEDLINE-20123838; Pubmed-10656762;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     288 ---- LGKGKGEPGQSDSALKTGKP 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG11 88:75/~766(1997).
MBL; U78598; AAC60114.1; ~.
INTERPIO; IPR000024; Fz. domain.
INTERPIO; IPR001134; Netrin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                            Pfam; PF01759; NTR; 1.
SMART; SM00063; FRI; 1.
PROSITE; PS50038; FZ; 1
SEQUENCE 315 AA; 350
                                                                                                                                                                                                                                            Pfam; PF01392; Fz; 1.
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                                                                                                                         Francis-West P.H.;
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                   NCBI_TaxID-9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Frzb precursor,
                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 LACDELPVYDRGVCISPEAIVT----DLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRC 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Agchosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238 YTTSGCLCPPLTVNEEYVIMGYEDEERSRLLLVEGSIAEKWKDRLGKVKKVRWDMKLRHLG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 KCKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSS-SPIPRTQVPL 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 ITNSSCOCPHILPHODVLIMCY -- EWRSRMMLLENCLVEKWRDQLSKRSIQWEERLQ ---
                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 44.1%; Score 829; DB 11; Length 32
Best Local Similarity 51.1%; Pred. No. 8.2e-68;
Matches 166; Conservative 49; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                    the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC016884, AAH16884.1; -.
MCD; MGI:89203; Frzb.
InterPro; IPR000024; Fz_domain.
InterPro; IPR001134; Netrin_C.
Pfam; PF01392; Frz 1.
Pfam; PF01392; Frz 1.
PROSITE; PS50038; Fz; 1.
SEQUENCE 323 AA; 36039 MW; 3F1449EBCFC97740 CRC64;
                                                                                                                                                                          Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
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                                                                                                                       323
                                                                                                                                                           Created)
                                                                                                                         PRT;
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                                                                                                                    091W58 PRELIMINARY;
091W58;
01-DEC-2001 (TrEMBLrel. 19, Cr
01-DEC-2001 (TrEMBLrel. 19, Le
01-JUN-2002 (TrEMBLrel. 21, Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2001 (TrEMBLrel. 18,
PRELIMINARY;
                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                  TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   091A95
                                                                                    RESULT 7
                                                                                                       091W5B
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170 CKRLSPDRCKCKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSS-S 228
                                                                                                                                                                                                                                      61 YEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESLACDELPVYDRGVCISPEAIV-TDLPEDVKWIDI-----TPDMMVQERPLD---VD 169
                                                                                                                                                     261 --WRSRMMLLENCLVEKWRDQLSKRSIQWEERLQEQRRTVQDKKKTAGRTSRSNPPKPKG 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 KIKAVORSGCNEVTTVVDVKEIFKSS-SPIPRTQVPLITNSSCQCPHILPHQDVLIMCYE
    29 ASCEPVRIPMCKSMPWNWTKMPNHLHHSTQANAILAIEQFEGLLTTECSQDLLFFLCAMY
                                                                                                                               142 IVTDLPEDVKWIDITPDMMVQERPLDVDCKRLSPDRCKCKKVKPTLATYLSKNYSYVIHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Furutani-Seiki M.; "Cloning of zebrafish fzb-1, antagonizer of Wnt signaling."; Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shinya M., Driever W., Furutani-Seiki M.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF116853; AAD22462.1; ...
ZIN; ZDB-GENE-990715-1; fzbl.
InterPro; IPR00024; Fz_domain.
InterPro; IPR00134; Netrin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36031 MW; 0F23DFF09F9B9414 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.5%; Score 799; DB 13; 50.2%; Pred. No. 4.5e-65;
                                                                                                                                                                                                                                                                                                                                           261 DKERTRLLLVEGSLAEKWRDRLAKKVKRWDQKLRR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                  319 KPPAPKPASPKKNIKTRSAQ 338
                                                                                                                                                                                                                                                                                                                                                                                                            301 DPVAP---IPNKNSNSRQAR 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, 01-DEC-2001 (TrEMBLrel. 19,
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Pfam; PF01759; NTR; 1.
SMART; SM00063; FRI; 1
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NCBI_TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                    142 IVTDLPEDVKWIDITPDMMVQERPLDV - - DCKRLSPDRCKCKKVKPTLATYLSKNYSYV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 IHAKIKAVQRSGCNEVTTVVDVKEIFKSS-SPIPRTQVPLITNSSCQCPH1LPHQDVLIM 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            258 CYE--WRSRMMILENCIVEKWRDQLSKRSIQWEERLQEQRRTVQDKKKTAGRTSRSNPPK 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 APCEAVRIPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEELVDVNCSAVLRFFFCAMY 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leyns L., Bouwmeester T., Kim S.H., Piccolo S., De Robertis E.M.; "Frzb-1 is a secreted antagonist of Wnt signaling expressed in the
                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Amphibia, Batrachia, Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                  43.8%; Score 822.5; DB 13; Length 319; llarity 50.2%; Pred. No. 3.2e-67; Conservative 49; Mismatches 73; Indels 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 318;
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                                                                                                         FRZB.
6E2F206E3DECB080 CRC64;
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Last annotation update)
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                                                                                     POTENTIAL
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SEQUENCE FROM N.A.
MEDLINE-97236495; Pubmed-9118218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 PKGKPPAPKPASPKKNIKTRSAQ 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 KSKDPVAP---IPNKNSNSRQAR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spenann organizer.";
Cell 88:747-756(1997).
EMBL: U68059; AAC60113.1; ...
InterPro; IPR000024; Fz. domain.
InterPro; IPR001134; Netrin_C.
                                                                              28 PO
319 FR
36062 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 161; Conservative
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Pfam; PF01759; NTR; 1.
SMART; SM00063; FRI; 1.
PROSITE; PS50038; FZ; 1.
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Pfam; PF01759; NTR; 1.
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PROSITE; PS50038; FZ;
                                                                                                       29 3
319 AA;
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                                                                                                                                                                                      Best Local Similarity
Matches 162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=8355;
                                                                                                       CHAIN
SEQUENCE
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SEQUENCE
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2001 (TrEMBLrel. 13, Last sequence update)
Secreted frizzled-related protein (Fragment).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                            61 YEELVDVNCSSVLRFFLCAMYAPICTLEFLHDDIKPCKSVCQRARDDCEPLMKMYNHSWP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLMKMYNHSWP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                       STRAIN-129/SVCP;
MEDLINE-21378144; PubMed-11485313;
Yam J. M.P., Chan K.W., Wong V.K.W., Hsiao W.L.W.;
Yam J. M.P., Chan K.W., Wong V.K.W., Hsiao W.L.W.;
Yaranscriptional activity of the promoter region of rat frizzled-
related protein gene.";
Biochem. Biophys. Res. Commun. 286:94-100(2001).
EMBL; AF364906; AAL14904.1;
InterPro; IPR000024; Fz_domain.
                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 PIPRTOVPLITNSSCOCPHILPHODVLIMCY--EWRSRMMLLENCLVEKWRDQLSKRSIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MFLSILVALCLWLHLALGVRGAPCEAVRIPMCRHMPWN1TRMPNHLHHSTQENAILAIEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                               Score 791; DB 11; Length 148;
Pred. No. 1e-64;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  * NON_TER 148 148 SEQUENCE 148 AA; 16940 MW; 13D7CED1960B3092 CRC64;
                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       213 AA,
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                                                                                                                                                                                                      Frizzled-related protein 4 (Fragment) FRP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                42.18;
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STRAIN-BREED WHITE LEGHORN;
                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01392; Fz; 1.
PROSITE; PS50038; Fz; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 143; Conservative
                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                        287 WEERLQEOR 295
                                                                                             301 WDOAANGRR 309
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         NCBI_TaxID-10090;
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Best Local
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Q9PTD9
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Baranski M., Berdougo E., Sandler J., Darnell D.K., Burrus L.W.;
"The Dynamic Expression Pattern of frzb-1 Suggests Multiple Roles in Chick Development."

EMBL, AF207665; AAF20143.1; -.
InterPro; IPR000024; Fz_domain.
InterPro; IPR000134; Netrin_C.
Pfam; PF01392; Fz; 1.
Pfam; PF01392; Fz; 1.
Pfam; PF01759; NTR: 1.
NONATE: PS50038; Fz; 1.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97 CKSVCQRARDDCEPLMKMYNHSWPESLACDELPVYDRGVCISPEAIVTDLPEDVKWIDIT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 PDMMVQERPLDV---DCKRI,SPDRCKCKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53 NAILAIEQYEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKPCKSVCQRARDDCEPLM 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 WNITRMPNHLHHSTQENAILAIEQYEELVDVNCSAVLRFFFCAMYAPICTLEFLHDPIKP 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BHKFIZ.

Bukasocricetus auratus (Golden hamster).

Bukaryota: Metazoa: Chordata; Cranlata: Vertebrata; Euteleostomi;

Mammalia: Butheria: Rodentia; Sciurognathi; Muridae; Cricetinae;
                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.8%; Score 673.5; DB 13; Length 213; Best Local Similarity 56.1%; Pred. No. 8.7e-54; Matches 128; Conservative 32; Mismatches 49; Indels 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 33.1%; Score 621.5; DB 11; Length 261; Best Local Similarity 47.0%; Pred. No. 6.4e-49; Matches 131; Conservative 42; Mismatches 73; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-97321551; PubMed-9178261;
Mayr T., Deutsch U., Kuhl M., Drexler H.C.A., Lottspelch F.,
Deutzmann R., Wedlich D., Risau W.;
"Fritz; a secreted frizzled-related protein that inhibits Wnt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                214 VITVVDVKEIFKSS-SPIPRTQVPLITNSSCQCPHILPHQDVLIMCYE 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213
23766 MW; E30E237339FD27E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 AA; 29347 MW; BED383DCC70203C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                             213 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fritz (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10036;
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                                     171 -KRLSPDRCKCKKVKPTLATYLSKNYSYVIHAKIKAVQRSGCNEVTTVVDVKEIFKSS-S 228
                                                                                                          229 PIPRTQVPLITNSSCQCPHILPHQDVLIMCY -- EWRSRAMALLENCLVEKWRDQLSKRSIQ 286
                                                                                                                                                              2 NXILXIXQFEGLLXTHCXGDLLFFLCAMYAPICTXDFQREPIRPCKSVCERARQGCEPIL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 IPMCRHMPWNITRMPNHLHHSTQENAILAIEQYEELVDVNCSAVLRFFFCAMYAPICTLE 88
                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 27.2%; Score 512; DB 6; Length 130; Best Local Similarity 71.2%; Pred. No. 3e-39; Matches 89; Conservative 15; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

TISSUE-KNEE ARTICULAR CARTILAGE;

KALACAKA H., Enomato K.,

Kalacaka H., Enomato K.,

Submittal cDNA sequence isolated by RT-PCR.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL, AB073103; BAB69964.1;

InterPro; IPR000024; Fz_domain.

Pfam; PF01992; Fz; 1.
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NON_TER 130 130
SEQUENCE 130 AA; 14486 MW; 9B39193BF2674721 CRC64;
                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Frizzled protein homolog (Fragment).
                                                                                                                                                                                                                  287 WEERLQ------EQRRIVQDKKKTAGRISRSNPPKPKG 318
                                                                                                                                                                                                                                                                                                130 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: March 7, 2003, 11:24:59
Job time: 38 secs
                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 DLPED 149
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                                                                                                                                                                                                                                                                                                              095JB1;
                                                                                                                                                                                                                                                                                               Q95JB1
                                                                                                                                                                                                                                                                   RESULT 15
Q95JB1
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infusion vs. oral - anabonent

variation between mamm.

h-003 Sept. 2000 bovins

are all mamm. described